

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gallatin, W. Michael
Kilgannon, Patrick D.
- (ii) TITLE OF INVENTION: ICAM-4 Materials and Methods
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 233 South Wacker Drive, 6300 Sears Tower
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/827,689
 - (B) FILING DATE: 27-JAN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/889,724
 - (B) FILING DATE: 26-MAY-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/894,061
 - (B) FILING DATE: 05-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/009,266
 - (B) FILING DATE: 22-JAN-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/102,852
 - (B) FILING DATE: 05-AUG-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/245,295
 - (B) FILING DATE: 18-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/485,604
 - (B) FILING DATE: 07-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: WILLIAMS, JR. JOSEPH A.
 - (B) REGISTRATION NUMBER: 38,659
 - (C) REFERENCE/DOCKET NUMBER: 27866/33321

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 312-474-6300
- (B) TELEFAX: 312-474-0448
- (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 61..2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCGATCA CTCGCGCTCC CCTCGCCTTC TGCGCTCTCC CCTCCCTGGC AGCGGCGGCA	60
ATG CCG GGG CCT TCA CCA GGG CTG CGC CGA ACG CTC CTC GGC CTC TGG	108
Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Thr Leu Leu Gly Leu Trp	
1 5 10 15	
GCT GCC CTG GGC CTG GGG ATC CTA GGC ATC TCA GCG GTC GCG CTA GAA	156
Ala Ala Leu Gly Leu Gly Ile Leu Gly Ile Ser Ala Val Ala Leu Glu	
20 25 30	
CCT TTC TGG GCG GAC CTT CAG CCC CGC GTG GCG CTC GTG GAG CGC GGG	204
Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Leu Val Glu Arg Gly	
35 40 45	
GGC TCG CTG TGG CTC AAC TGC AGC ACT AAC TGT CCG AGG CCG GAG CGC	252
Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg	
50 55 60	
GGT GGC CTG GAG ACC TCG CTA CGC CGA AAC GGG ACC CAG AGG GGT CTG	300
Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu	
65 70 75 80	
CGC TGG CTG GCT CGA CAG CTG GTG GAC ATC CGA GAG CCT GAA ACC CAG	348
Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln	
85 90 95	
CCG GTC TGC TTC TTC CGC TGC GCG CGC CGC ACA CTC CAA GCG CGT GGG	396
Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly	
100 105 110	
CTC ATC CGA ACT TTC CAG CGA CCG GAT CGG GTA GAG CTA GTG CCT CTG	444
Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Val Pro Leu	
115 120 125	
CCT CCT TGG CAG CCT GTA GGT GAG AAC TTC ACC TTG AGC TGC AGG GTC	492
Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val	
130 135 140	
CCG GGG GCA GGA CCC CGA GCG AGC CTC ACA TTG ACC TTG CTG CGA GGC	540
Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly	
145 150 155 160	

GGC Gly	CAG Gln	GAG Glu	CTG Leu	ATT Ile 165	CGC Arg	CGA Arg	AGT Ser	TTC Phe	GTA Val 170	GGC Gly	GAG Glu	CCA Pro	CCC Pro	CGA Arg 175	GCT Ala	588
CGG Arg	GGT Gly	GCG Ala	ATG Met 180	CTC Leu	ACC Thr	GCC Ala	ACG Thr	GTC Val 185	CTG Leu	GCG Ala	CGC Arg	AGA Arg	GAG Glu 190	GAT Asp	CAC His	636
AGG Arg	GCC Ala	AAT Asn 195	TTC Phe	TCA Ser	TGC Cys	CTC Leu	GCG Ala 200	GAG Glu 200	CTT Leu	GAC Asp	CTG Leu	CGG Arg 205	CCA Pro	CAC His	GGC Gly	684
TTG Leu	GGA Gly 210	CTG Leu	TTT Phe	GCA Ala	AAC Asn 215	AGC Ser	TCA Ser	GCC Ala	CCC Pro	AGA Arg	CAG Gln 220	CTC Leu	CGC Arg	ACG Thr	TTT Phe	732
GCC Ala 225	ATG Met	CCT Pro	CCA Pro	CTT Leu 230	TCC Ser	CCG Pro	AGC Ser	CTT Leu	ATT Ile 235	GCC Ala 235	CCA Pro	CGA Arg	TTC Phe	TTA Leu	GAA Glu 240	780
GTG Val	GGC Gly	TCA Ser	GAA Glu 245	AGG Arg	CCG Pro	GTG Val	ACT Thr	TGC Cys	ACT Thr 250	TTG Leu	GAT Asp	GGA Gly	CTG Leu	TTT Phe 255	CCT Pro	828
GCC Ala	CCA Pro	GAA Glu 260	GCC Ala	GGG Gly	GTT Val	TAC Tyr	CTC Leu	TCT Ser 265	CTG Leu	GGA Gly	GAT Asp	CAG Gln 270	AGG Arg	CTT Leu	CAT His	876
CCT Pro	AAT Asn 275	GTG Val	ACC Thr	CTC Leu	GAC Asp	GGG Gly	GAG Glu 280	AGC Ser	CTT Leu	GTG Val	GCC Ala 285	ACT Thr	GCC Ala	ACA Thr	GCT Ala	924
ACA Thr 290	GCA Ala	AGT Ser	GAA Glu	GAA Glu	CAG Gln	GAA Glu 295	GGC Gly	ACC Thr	AAA Lys	CAG Gln 300	CTG Leu	ATG Met	TGC Cys	ATC Ile	GTG Val	972
ACC Thr 305	CTC Leu	GGG Gly	GGC Gly	GAA Glu 310	AGC Ser	AGG Arg	GAG Glu	ACC Thr	CAG Gln	GAA Glu 315	AAC Asn	CTG Leu	ACT Thr	GTC Val	TAC Tyr 320	1020
AGC Ser	TTC Phe	CCG Pro	GCT Ala 325	CCT Pro	CTT Leu	CTG Leu	ACT Thr	TTA Leu	AGT Ser 330	GAG Glu	CCA Pro	GAA Glu	GCC Ala 335	CCC Pro	GAG Glu	1068
GGA Gly	AAG Lys	ATG Met 340	GTG Val	ACC Thr	GTA Val	AGC Ser	TGC Cys	TGG Trp 345	GCA Ala	GGG Gly	GCC Ala	CGA Arg	GCC Ala 350	CTT Leu	GTC Val	1116
ACC Thr	TTG Leu 355	GAG Glu	GGA Gly	ATT Ile	CCA Pro	GCT Ala 360	GCG Ala	GTC Val	CCT Pro	GGG Gly	CAG Gln	CCC Pro 365	GCT Ala	GAG Glu	CTC Leu	1164
CAG Gln 370	TTA Leu	AAT Asn	GTC Val	ACA Thr	AAG Lys	AAT Asn 375	GAC Asp	GAC Asp	AAG Lys	CGG Arg	GGC Gly 380	TTC Phe	TTC Phe	TGC Cys	GAC Asp	1212
GCT Ala 385	GCC Ala	CTC Leu	GAT Asp	GTG Val	GAC Asp 390	GGG Gly	GAA Glu	ACT Thr	CTG Leu	AGA Arg 395	AAG Lys	AAC Asn	CAG Gln	AGC Ser	TCT Ser 400	1260
GAG Glu	CTT Leu	CGT Arg	GTT Val	CTG Leu 405	TAC Tyr	GCA Ala	CCT Pro	CGG Arg	CTG Leu 410	GAT Asp	GAC Asp	TTG Leu	GAC Asp	TGT Cys	CCC Pro 415	1308

AGG	AGC	TGG	ACG	TGG	CCA	GAG	GGT	CCA	GAG	CAG	ACC	CTC	CAC	TGC	GAG	1356
Arg	Ser	Trp	Thr	Trp	Pro	Glu	Gly	Pro	Glu	Gln	Thr	Leu	His	Cys	Glu	
			420					425					430			
GCC	CGT	GGA	AAC	CCT	GAG	CCC	TCC	GTG	CAC	TGT	GCA	AGG	CCT	GAC	GGT	1404
Ala	Arg	Gly	Asn	Pro	Glu	Pro	Ser	Val	His	Cys	Ala	Arg	Pro	Asp	Gly	
		435					440					445				
GGG	GCG	GTG	CTA	GCG	CTG	GGC	CTG	TTG	GGT	CCA	GTG	ACC	CGT	GCC	CTC	1452
Gly	Ala	Val	Leu	Ala	Leu	Gly	Leu	Leu	Gly	Pro	Val	Thr	Arg	Ala	Leu	
	450					455					460					
GCG	GGC	ACT	TAC	CGA	TGT	ACA	GCA	ATC	AAT	GGG	CAA	GGC	CAG	GCG	GTC	1500
Ala	Gly	Thr	Tyr	Arg	Cys	Thr	Ala	Ile	Asn	Gly	Gln	Gly	Gln	Ala	Val	
465					470				475						480	
AAG	GAT	GTG	ACC	CTG	ACT	GTG	GAA	TAT	GCC	CCA	GCG	CTG	GAC	AGT	GTA	1548
Lys	Asp	Val	Thr	Leu	Thr	Val	Glu	Tyr	Ala	Pro	Ala	Leu	Asp	Ser	Val	
				485					490					495		
GGC	TGC	CCA	GAA	CGT	ATT	ACT	TGG	CTG	GAG	GGG	ACA	GAG	GCA	TCG	CTT	1596
Gly	Cys	Pro	Glu	Arg	Ile	Thr	Trp	Leu	Glu	Gly	Thr	Glu	Ala	Ser	Leu	
		500					505						510			
AGC	TGT	GTG	GCA	CAC	GGG	GTC	CCA	CCA	CCT	AGC	GTG	AGC	TGT	GTG	CGC	1644
Ser	Cys	Val	Ala	His	Gly	Val	Pro	Pro	Pro	Ser	Val	Ser	Cys	Val	Arg	
		515					520					525				
TCT	GGA	AAG	GAG	GAA	GTC	ATG	GAA	GGG	CCC	CTG	CGT	GTG	GCC	CGG	GAG	1692
Ser	Gly	Lys	Glu	Glu	Val	Met	Glu	Gly	Pro	Leu	Arg	Val	Ala	Arg	Glu	
	530					535					540					
CAC	GCT	GGC	ACT	TAC	CGA	TGC	GAA	GCC	ATC	AAC	GCC	AGG	GGA	TCA	GCG	1740
His	Ala	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ile	Asn	Ala	Arg	Gly	Ser	Ala	
545					550					555					560	
GCC	AAA	AAT	GTG	GCT	GTC	ACG	GTG	GAA	TAT	GGT	CCC	AGT	TTT	GAG	GAG	1788
Ala	Lys	Asn	Val	Ala	Val	Thr	Val	Glu	Tyr	Gly	Pro	Ser	Phe	Glu	Glu	
			565						570					575		
TTG	GGC	TGC	CCC	AGC	AAC	TGG	ACT	TGG	GTA	GAA	GGA	TCT	GGA	AAA	CTG	1836
Leu	Gly	Cys	Pro	Ser	Asn	Trp	Thr	Trp	Val	Glu	Gly	Ser	Gly	Lys	Leu	
			580					585					590			
TTT	TCC	TGT	GAA	GTT	GAT	GGG	AAG	CCG	GAA	CCA	CGC	GTG	GAG	TGC	GTG	1884
Phe	Ser	Cys	Glu	Val	Asp	Gly	Lys	Pro	Glu	Pro	Arg	Val	Glu	Cys	Val	
		595					600					605				
GGC	TCG	GAG	GGT	GCA	AGC	GAA	GGG	GTA	GTG	TTG	CCC	CTG	GTG	TCC	TCG	1932
Gly	Ser	Glu	Gly	Ala	Ser	Glu	Gly	Val	Val	Leu	Pro	Leu	Val	Ser	Ser	
	610					615					620					
AAC	TCT	GGT	TCC	AGA	AAC	TCT	ATG	ACT	CCT	GGT	AAC	CTG	TCA	CCG	GGT	1980
Asn	Ser	Gly	Ser	Arg	Asn	Ser	Met	Thr	Pro	Gly	Asn	Leu	Ser	Pro	Gly	
625					630					635					640	
ATT	TAC	CTC	TGC	AAC	GCC	ACC	AAC	CGG	CAT	GGC	TCC	ACA	GTC	AAA	ACA	2028
Ile	Tyr	Leu	Cys	Asn	Ala	Thr	Asn	Arg	His	Gly	Ser	Thr	Val	Lys	Thr	
				645					650					655		
GTC	GTC	GTG	AGC	GCG	GAA	TCA	CCG	CCA	CAG	ATG	GAT	GAA	TCC	AGT	TGC	2076
Val	Val	Val	Ser	Ala	Glu	Ser	Pro	Pro	Gln	Met	Asp	Glu	Ser	Ser	Cys	
			660					665					670			

CAG CTG ACA TCT TCC TGAGCCTGTA TCCAGCTCCC CCAGGGGCCCT CGAAAGCACA 2851
Gln Leu Thr Ser Ser
915

GGGGTGGACG TATGTATTGT TCACTCTCTA TTTATTCAAC TCCAGGGGCG TCGTCCCCGT	2911
TTTCTACCCA TTCCCTTAAT AAAGTTTTTA TAGGAGAAAA AAAAAAAAAA AAAAAAAAAA	2971
AAAAAAAAAA AAAAAA	2988

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gly	Pro	Ser	Pro	Gly	Leu	Arg	Arg	Thr	Leu	Leu	Gly	Leu	Trp
1				5					10					15	
Ala	Ala	Leu	Gly	Leu	Gly	Ile	Leu	Gly	Ile	Ser	Ala	Val	Ala	Leu	Glu
		20						25					30		
Pro	Phe	Trp	Ala	Asp	Leu	Gln	Pro	Arg	Val	Ala	Leu	Val	Glu	Arg	Gly
		35					40					45			
Gly	Ser	Leu	Trp	Leu	Asn	Cys	Ser	Thr	Asn	Cys	Pro	Arg	Pro	Glu	Arg
	50					55					60				
Gly	Gly	Leu	Glu	Thr	Ser	Leu	Arg	Arg	Asn	Gly	Thr	Gln	Arg	Gly	Leu
65					70					75					80
Arg	Trp	Leu	Ala	Arg	Gln	Leu	Val	Asp	Ile	Arg	Glu	Pro	Glu	Thr	Gln
				85					90					95	
Pro	Val	Cys	Phe	Phe	Arg	Cys	Ala	Arg	Arg	Thr	Leu	Gln	Ala	Arg	Gly
			100					105					110		
Leu	Ile	Arg	Thr	Phe	Gln	Arg	Pro	Asp	Arg	Val	Glu	Leu	Val	Pro	Leu
	115						120					125			
Pro	Pro	Trp	Gln	Pro	Val	Gly	Glu	Asn	Phe	Thr	Leu	Ser	Cys	Arg	Val
	130					135					140				
Pro	Gly	Ala	Gly	Pro	Arg	Ala	Ser	Leu	Thr	Leu	Thr	Leu	Leu	Arg	Gly
145					150					155					160
Gly	Gln	Glu	Leu	Ile	Arg	Arg	Ser	Phe	Val	Gly	Glu	Pro	Pro	Arg	Ala
			165						170					175	
Arg	Gly	Ala	Met	Leu	Thr	Ala	Thr	Val	Leu	Ala	Arg	Arg	Glu	Asp	His
			180					185					190		
Arg	Ala	Asn	Phe	Ser	Cys	Leu	Ala	Glu	Leu	Asp	Leu	Arg	Pro	His	Gly
		195					200					205			
Leu	Gly	Leu	Phe	Ala	Asn	Ser	Ser	Ala	Pro	Arg	Gln	Leu	Arg	Thr	Phe
	210					215					220				
Ala	Met	Pro	Pro	Leu	Ser	Pro	Ser	Leu	Ile	Ala	Pro	Arg	Phe	Leu	Glu
225					230					235					240

Val Gly Ser Glu Arg Pro Val Thr Cys Thr Leu Asp Gly Leu Phe Pro
245 250 255

Ala Pro Glu Ala Gly Val Tyr Leu Ser Leu Gly Asp Gln Arg Leu His
260 265 270

Pro Asn Val Thr Leu Asp Gly Glu Ser Leu Val Ala Thr Ala
275 280 285

Thr Ala Ser Glu Glu Gln Glu Gly Thr Lys Gln Leu Met Cys Ile Val
290 295 300

Thr Leu Gly Gly Glu Ser Arg Glu Thr Gln Glu Asn Leu Thr Val Tyr
305 310 315 320

Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Glu Ala Pro Glu
325 330 335

Gly Lys Met Val Thr Val Ser Cys Trp Ala Gly Ala Arg Ala Leu Val
340 345 350

Thr Leu Glu Gly Ile Pro Ala Ala Val Pro Gly Gln Pro Ala Glu Leu
355 360 365

Gln Leu Asn Val Thr Lys Asn Asp Asp Lys Arg Gly Phe Phe Cys Asp
370 375 380

Ala Ala Leu Asp Val Asp Gly Glu Thr Leu Arg Lys Asn Gln Ser Ser
385 390 395 400

Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Leu Asp Cys Pro
405 410 415

Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu His Cys Glu
420 425 430

Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Pro Asp Gly
435 440 445

Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu
450 455 460

Ala Gly Thr Tyr Arg Cys Thr Ala Ile Asn Gly Gln Gly Gln Ala Val
465 470 475 480

Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val
485 490 495

Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu
500 505 510

Ser Cys Val Ala His Gly Val Pro Pro Pro Ser Val Ser Cys Val Arg
515 520 525

Ser Gly Lys Glu Glu Val Met Glu Gly Pro Leu Arg Val Ala Arg Glu
530 535 540

His Ala Gly Thr Tyr Arg Cys Glu Ala Ile Asn Ala Arg Gly Ser Ala
545 550 555 560

Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Ser Phe Glu Glu
565 570 575

Leu	Gly	Cys	Pro	Ser	Asn	Trp	Thr	Trp	Val	Glu	Gly	Ser	Gly	Lys	Leu
			580					585					590		
Phe	Ser	Cys	Glu	Val	Asp	Gly	Lys	Pro	Glu	Pro	Arg	Val	Glu	Cys	Val
		595					600					605			
Gly	Ser	Glu	Gly	Ala	Ser	Glu	Gly	Val	Val	Leu	Pro	Leu	Val	Ser	Ser
	610					615					620				
Asn	Ser	Gly	Ser	Arg	Asn	Ser	Met	Thr	Pro	Gly	Asn	Leu	Ser	Pro	Gly
	625				630					635					640
Ile	Tyr	Leu	Cys	Asn	Ala	Thr	Asn	Arg	His	Gly	Ser	Thr	Val	Lys	Thr
				645					650					655	
Val	Val	Val	Ser	Ala	Glu	Ser	Pro	Pro	Gln	Met	Asp	Glu	Ser	Ser	Cys
			660					665					670		
Pro	Ser	His	Gln	Thr	Trp	Leu	Glu	Gly	Ala	Glu	Ala	Thr	Ala	Leu	Ala
		675					680					685			
Cys	Ser	Ala	Arg	Gly	Arg	Pro	Ser	Pro	Arg	Val	Arg	Cys	Ser	Arg	Glu
	690					695					700				
Gly	Ala	Ala	Arg	Leu	Glu	Arg	Leu	Gln	Val	Ser	Arg	Glu	Asp	Ala	Gly
	705				710					715					720
Thr	Tyr	Leu	Cys	Val	Ala	Thr	Asn	Ala	His	Gly	Thr	Asp	Ser	Arg	Thr
				725					730					735	
Val	Thr	Val	Gly	Val	Glu	Tyr	Arg	Pro	Val	Val	Ala	Glu	Leu	Ala	Ala
			740					745					750		
Ser	Pro	Pro	Ser	Val	Arg	Pro	Gly	Gly	Asn	Phe	Thr	Leu	Thr	Cys	Arg
		755					760					765			
Ala	Glu	Ala	Trp	Pro	Pro	Ala	Gln	Ile	Ser	Trp	Arg	Ala	Pro	Pro	Gly
	770					775					780				
Ala	Leu	Asn	Leu	Gly	Leu	Ser	Ser	Asn	Asn	Ser	Thr	Leu	Ser	Val	Ala
	785				790					795					800
Gly	Ala	Met	Gly	Ser	His	Gly	Gly	Glu	Tyr	Glu	Cys	Ala	Ala	Thr	Asn
				805					810					815	
Ala	His	Gly	Arg	His	Ala	Arg	Arg	Ile	Thr	Val	Arg	Val	Ala	Gly	Pro
			820					825					830		
Trp	Leu	Trp	Val	Ala	Val	Gly	Gly	Ala	Ala	Gly	Gly	Ala	Ala	Leu	Leu
		835					840					845			
Ala	Ala	Gly	Ala	Gly	Leu	Ala	Phe	Tyr	Val	Gln	Ser	Thr	Ala	Cys	Lys
	850					855					860				
Lys	Gly	Glu	Tyr	Asn	Val	Gln	Glu	Ala	Glu	Ser	Ser	Gly	Glu	Ala	Val
	865				870					875					880
Cys	Leu	Asn	Gly	Ala	Gly	Gly	Thr	Pro	Gly	Ala	Glu	Gly	Gly	Ala	Glu
				885					890					895	
Thr	Pro	Gly	Thr	Ala	Glu	Ser	Pro	Ala	Asp	Gly	Glu	Val	Phe	Ala	Ile
			900					905					910		

Gln Leu Thr Ser Ser
915

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCG	GAT	CGG	GTA	GAG	CTA	GTG	CCT	CTG	CCT	CCT	TGG	CAG	CCT	GTA	GGT	48
Pro	Asp	Arg	Val	Glu	Leu	Val	Pro	Leu	Pro	Pro	Trp	Gln	Pro	Val	Gly	
1				5				10						15		
GAG	AAC	TTC	ACC	TTG	AGC	TGC	AGG	GTC	CCG	GGG	GCA	GGA	CCC	CGA	GCG	96
Glu	Asn	Phe	Thr	Leu	Ser	Cys	Arg	Val	Pro	Gly	Ala	Gly	Pro	Arg	Ala	
			20					25					30			
AGC	CTC	ACA	TTG	ACC	TTG	CTG	CGA	GGC	GGA	CAG	GAG	CTG	ATT	CGC	CGA	144
Ser	Leu	Thr	Leu	Thr	Leu	Leu	Arg	Gly	Gly	Gln	Glu	Leu	Ile	Arg	Arg	
			35				40					45				
AGT	TTC	GTA	GGC	GAG	CCA	CCC	CGA	GCT	CGG	TGT	GCG	ATG	CTC	ACC	GCC	192
Ser	Phe	Val	Gly	Glu	Pro	Pro	Arg	Ala	Arg	Cys	Ala	Met	Leu	Thr	Ala	
			50				55					60				
ACG	GTC	CTG	GCG	CGC	AGA	GAG	GAT	CAC	AGG	GAC	AAT	TTC	TCA	TGC	CTC	240
Thr	Val	Leu	Ala	Arg	Arg	Glu	Asp	His	Arg	Asp	Asn	Phe	Ser	Cys	Leu	
			65			70				75					80	
GCG	GAG	CTT	GAC	CTG	CGG	ACA	CAC	GGC	TTG	GGA	CTG	TTT	GCA	AAC	AGC	288
Ala	Glu	Leu	Asp	Leu	Arg	Thr	His	Gly	Leu	Gly	Leu	Phe	Ala	Asn	Ser	
			85						90					95		
TCA	GCC	CCC	AGA	CAG	CTC	CGC	ACG	TTT								315
Ser	Ala	Pro	Arg	Gln	Leu	Arg	Thr	Phe								
			100					105								

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1781 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 16..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCTCTCTG TCAGA ATG GCC ACC ATG GTA CCA TCC GTG TTG TGG CCC AGG	51
Met Ala Thr Met Val Pro Ser Val Leu Trp Pro Arg	
1 5 10	
GCC TGC TGG ACT CTG CTG GTC TGC TGT CTG CTG ACC CCA GGT GTC CAG	99
Ala Cys Trp Thr Leu Leu Val Cys Cys Leu Leu Thr Pro Gly Val Gln	
15 20 25	
GGG CAG GAG TTC CTT TTG CGG GTG GAG CCC CAG AAC CCT GTG CTC TCT	147
Gly Gln Glu Phe Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser	
30 35 40	
GCT GGA GGG TCC CTG TTT GTG AAC TGC AGT ACT GAT TGT CCC AGC TCT	195
Ala Gly Gly Ser Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser	
45 50 55 60	
GAG AAA ATC GCC TTG GAG ACG TCC CTA TCA AAG GAG CTG GTG GCC AGT	243
Glu Lys Ile Ala Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser	
65 70 75	
GGC ATG GGC TGG GCA GCC TTC AAT CTC AGC AAC GTG ACT GGC AAC AGT	291
Gly Met Gly Trp Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser	
80 85 90	
CGG ATC CTC TGC TCA GTG TAC TGC AAT GGC TCC CAG ATA ACA GGC TCC	339
Arg Ile Leu Cys Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser	
95 100 105	
TCT AAC ATC ACC GTG TAC GGG CTC CCG GAG CGT GTG GAG CTG GCA CCC	387
Ser Asn Ile Thr Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro	
110 115 120	
CTG CCT CCT TGG CAG CCG GTG GGC CAG AAC TTC ACC CTG CGC TGC CAA	435
Leu Pro Pro Trp Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln	
125 130 135 140	
GTG GAG GGT GGG TCG CCC CGG ACC AGC CTC ACG GTG GTG CTG CTT CGC	483
Val Glu Gly Gly Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg	
145 150 155	
TGG GAG GAG GAG CTG AGC CGG CAG CCC GCA GTG GAG GAG CCA GCG GAG	531
Trp Glu Glu Glu Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu	
160 165 170	
GTC ACT GCC ACT GTG CTG GCC AGC AGA GAC GAC CAC GGA GCC CCT TTC	579
Val Thr Ala Thr Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe	
175 180 185	
TCA TGC CGC ACA GAA CTG GAC ATG CAG CCC CAG GGG CTG GGA CTG TTC	627
Ser Cys Arg Thr Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe	
190 195 200	
GTG AAC ACC TCA GCC CCC CGC CAG CTC CGA ACC TTT GTG CTG CCC GTG	675
Val Asn Thr Ser Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val	
205 210 215 220	
ACC CCC CCG CGC CTC GTG GCC CCC CGG TTC TTG GAG GTG GAA ACG TCG	723
Thr Pro Pro Arg Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser	
225 230 235	
TGG CCG GTG GAC TGC ACC CTA GAC GGG CTT TTT CCA GCC TCA GAG GCC	771
Trp Pro Val Asp Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala	
240 245 250	

CAG	GTC	TAC	CTG	GCG	CTG	GGG	GAC	CAG	ATG	CTG	AAT	GCG	ACA	GTC	ATG	819
Gln	Val	Tyr	Leu	Ala	Leu	Gly	Asp	Gln	Met	Leu	Asn	Ala	Thr	Val	Met	
		255					260					265				
AAC	CAC	GGG	GAC	ACG	CTA	ACG	GCC	ACA	GCC	ACA	GCC	ACG	GCG	CGC	GCG	867
Asn	His	Gly	Asp	Thr	Leu	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Arg	Ala	
		270				275					280					
GAT	CAG	GAG	GGT	GCC	CGG	GAG	ATC	GTC	TGC	AAC	GTG	ACC	CTA	GGG	GGC	915
Asp	Gln	Glu	Gly	Ala	Arg	Glu	Ile	Val	Cys	Asn	Val	Thr	Leu	Gly	Gly	
285					290					295					300	
GAG	AGA	CGG	GAG	GCC	CGG	GAG	AAC	TTG	ACG	GTC	TTT	AGC	TTC	CTA	GGA	963
Glu	Arg	Arg	Glu	Ala	Arg	Glu	Asn	Leu	Thr	Val	Phe	Ser	Phe	Leu	Gly	
				305					310					315		
CCC	ATT	GTG	AAC	CTC	AGC	GAG	CCC	ACC	GCC	CAT	GAG	GGG	TCC	ACA	GTG	1011
Pro	Ile	Val	Asn	Leu	Ser	Glu	Pro	Thr	Ala	His	Glu	Gly	Ser	Thr	Val	
			320					325					330			
ACC	GTG	AGT	TGC	ATG	GCT	GGG	GCT	CGA	GTC	CAG	GTC	ACG	CTG	GAC	GGA	1059
Thr	Val	Ser	Cys	Met	Ala	Gly	Ala	Arg	Val	Gln	Val	Thr	Leu	Asp	Gly	
		335				340						345				
GTT	CCG	GCC	GCG	GCC	CCG	GGG	CAG	ACA	GCT	CAA	CTT	CAG	CTA	AAT	GCT	1107
Val	Pro	Ala	Ala	Ala	Pro	Gly	Gln	Thr	Ala	Gln	Leu	Gln	Leu	Asn	Ala	
	350					355					360					
ACC	GAG	AGT	GAC	GAC	GGA	CGC	AGC	TTC	TTC	TGC	AGT	GCC	ACT	CTC	GAG	1155
Thr	Glu	Ser	Asp	Asp	Gly	Arg	Ser	Phe	Phe	Cys	Ser	Ala	Thr	Leu	Glu	
365					370					375					380	
GTG	GAC	GGC	GAG	TTC	TTG	CAC	AGG	AAC	AGT	AGC	GTC	CAG	CTG	CGA	GTC	1203
Val	Asp	Gly	Glu	Phe	Leu	His	Arg	Asn	Ser	Ser	Val	Gln	Leu	Arg	Val	
				385					390					395		
CTG	TAT	GGT	CCC	AAA	ATT	GAC	CGA	GCC	ACA	TGC	CCC	CAG	CAC	TTG	AAA	1251
Leu	Tyr	Gly	Pro	Lys	Ile	Asp	Arg	Ala	Thr	Cys	Pro	Gln	His	Leu	Lys	
			400					405					410			
TGG	AAA	GAT	AAA	ACG	AGA	CAC	GTC	CTG	CAG	TGC	CAA	GCC	AGG	GGC	AAC	1299
Trp	Lys	Asp	Lys	Thr	Arg	His	Val	Leu	Gln	Cys	Gln	Ala	Arg	Gly	Asn	
		415					420					425				
CCG	TAC	CCC	GAG	CTG	CGG	TGT	TTG	AAG	GAA	GGC	TCC	AGC	CGG	GAG	GTG	1347
Pro	Tyr	Pro	Glu	Leu	Arg	Cys	Leu	Lys	Glu	Gly	Ser	Ser	Arg	Glu	Val	
	430					435					440					
CCG	GTG	GGG	ATC	CCG	TTC	TTC	GTC	AAC	GTA	ACA	CAT	AAT	GGT	ACT	TAT	1395
Pro	Val	Gly	Ile	Pro	Phe	Phe	Val	Asn	Val	Thr	His	Asn	Gly	Thr	Tyr	
445					450					455					460	
CAG	TGC	CAA	GCG	TCC	AGC	TCA	CGA	GGC	AAA	TAC	ACC	CTG	GTC	GTG	GTG	1443
Gln	Cys	Gln	Ala	Ser	Ser	Ser	Arg	Gly	Lys	Tyr	Thr	Leu	Val	Val	Val	
				465					470					475		
ATG	GAC	ATT	GAG	GCT	GGG	AGC	TCC	CAC	TTT	GTC	CCC	GTC	TTC	GTG	GCG	1491
Met	Asp	Ile	Glu	Ala	Gly	Ser	Ser	His	Phe	Val	Pro	Val	Phe	Val	Ala	
			480					485					490			
GTG	TTA	CTG	ACC	CTG	GGC	GTG	GTG	ACT	ATC	GTA	CTG	GCC	TTA	ATG	TAC	1539
Val	Leu	Leu	Thr	Leu	Gly	Val	Val	Thr	Ile	Val	Leu	Ala	Leu	Met	Tyr	
		495					500					505				

GTC TTC AGG GAG CAC CAA CGG AGC GGC AGT TAC CAT GTT AGG GAG GAG Val Phe Arg Glu His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu 510 515 520	1587
AGC ACC TAT CTG CCC CTC ACG TCT ATG CAG CCG ACA GAA GCA ATG GGG Ser Thr Tyr Leu Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly 525 530 535 540	1635
GAA GAA CCG TCC AGA GCT GAG TGACGCTGGG ATCCGGGATC AAAGTTGGCG Glu Glu Pro Ser Arg Ala Glu 545	1686
GGGGCTTGGC TGTGCCCTCA GATTCCGCAC CAATAAAGCC TTCAAACCTCC CAAAAAAAAA	1746
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA	1781

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGAACGCTC CTCGGCCTCT GGTCTNCTCT GGNCTGGGG ATCCTAGGCA TCTCAGGTAA	60
GAAGAGCCCG CCCGTGGAGC NAGGTGGATA AGGCGGGGGC GGAATTGAAG GACCAGAGAG	120
GGCGGCCCCG GTGTCCCCCT CCAGGCTCCG CCCTCTTCTA GCTTCCCACG CTTCTGTCAC	180
CACCTGGAGN TCGGGGCTTC TCCCCGTCCT TCCTCCACCC CAACACACCT CAATCTTTCA	240
GANCTGAACC CAGCACCTTT TCTGGANTNG GGGNNTTGCA CCTAACCTGT CTCAGGAGAN	300
ACTGTGGCTC TCCTGTCCTC TCCTGCTCTG TNATGCCCTA TGGTTCACAG ACTGGCATCA	360
TCCCTATTCA TGATCCTCAA AGACNCCATC TCCTCAACTG TCATAACTCA GAGCTCTATT	420
CCCCCTCCAC CTGGAGCCCT GGAAACCGGC TTTCTAGGGC TTTTCTCCGC GGTCTCTTCC	480
CGGAGTTCAG CGTTGTGGCT TTTTGTCCAA GTTACTCAAG TTTGGGGACA ATCTCCTTTA	540
AGCCTTTGAC TCAGTCTCAT TTCCACTTTG CTTTGGCCCC AAGCCTCTGT GTCTCTCCCC	600
CATTTCTGA CGATCTGTCA GAGTCTTAAG AGTGATTTGG TTCCCCATCC CCCCTCCAAC	660
TGGAGTCTCC TCCTCACTAT TGATGTGTGC ATCTGAGACC CCCATCCCCG CACCGAGTTT	720
CCCCATCTCT GTCAGTAAAG AGCAAGGCTT CCAGAGACAA CCCTCTAATA GCGCGTCAGT	780
CCCGAATCTT GAGTGGGATG CGGGACTCCC GTGCTATTTT TTGGCGGAGG TCTTTCCTGG	840
TCCTTATGGA CACCCCTGGT TTGGGATATG GGGGCCGCTA AGATTTTCTA GATGGGGTCC	900
CTAGGCTGAG NCCGCGTTTT CCCGGGCAGC GGTCGCGCTA GAACCTTTCT GGGCGGACCT	960
TCAGCCCCGC GTGGCGCTCG TGGAGCGCGG GGGCTCGCTG TGGCTCAACT GCAGCACTAA	1020
CTGTCCGAGG CCGGAGCGCG GTGGCCTGGA GACCTCGCTA CGCCGAAACG GGACCCAGAG	1080

GGGTCTGNAC TGNCTGGCTC GACAGCTGGT GGACATCCGA GANCCTGAAA CCCAGCCGGT	1140
CTGCTTCTTC CNCTGCGCGC GCCGCACACT CCAAGCGCGT GGGCTCATCC GAACTTTCCG	1200
TGAGTTCAGG GTGGGCACNC CCCTTGGGTC TCTGGACCTC CCCCTCAAGC TCCTCCCACC	1260
CGCCCTCTGA TCCTCCTGCT TGTCTGAAA GTACTACAGC TGGCTAGAGC GGAGTTTTTG	1320
GTCCCTTGCA GAGCGACCGG ATCGGGTAGA GCTAGTGCCT CTGCCTCCTT GGCAGCCTGT	1380
AGGTGAGAAC TTCACCTTGA GCTGCAGGGT CCCGGGGGCA GGACCCCGAG CGAGCCTCAC	1440
ATTGACCTTG CTGCGAGGCG GCCAGGAGCT GATTTCGCCGA AGTTTCGTAG GCGAGCCACC	1500
CCGAGCTCGG GGTGCGATGC TCACCGCCAC GGTCCTGGCG CGCAGAGAGG ATCACAGGGC	1560
CAATTTCTCA TGCCTCGCGG AGCTTGACCT GCGNCCACAC GGCTTGGGAC TGTTTGCANA	1620
CAGCTCAGCC CCCAGACAGC TCCGCACGTT TGGTGAGTGT GGACCCTAAC TGACAGATTT	1680
TAAGAAGTTT AGGGCAGCCA GCGGTGGTGG CATGGTGTCTG TAGGCCCTAA GTCCCAGCCC	1740
AAGCAGANCT AAGNCGGATC TCTTGTGAAT TAAAAGTCTA GCTCGTCTAC ATAACGAGGN	1800
CTGCATAGTT AAATCCCCCA AAAGTCTAAG CAGCTAGCCC TTACTTCCAA CACAAGTACT	1860
AGCTTAAGTA CTTTCTCCTG TGAGCTTTTT CTTTTATGTA TTTACTCGTT GAGAGAAAAA	1920
GAGAGTGTGT GTACGTGCCT TTATGCACAT GCCGCAGTGC TTGTATGGAA GTTAAAGAAT	1980
AAGGAGGCGT TCTGCCCTTC CATCCTGTGG GTCCTAGGGG TGGTATTAGC TCCTCAGGCT	2040
TTGTTAGTNA CAAGCGCCTA GGCTTGGGGA GCCATCTCGC CCGCTCCTCT GTATCTTTAG	2100
GGTGAAACCA GACAATGCAT GCAAATTGGT TGATCAACAC TGAATGTTTA GTTCGTAAAT	2160
TCAAGCTCTG TTCTTTGTCT TCCTCAGCCA TGCCTCCACT TTCCCCCGAG CCTTATTGCC	2220
CCACGATTCT TAGAAGTGGG CTCAGAAAGG CCGGTGACKT GCACTTTGGA TGGACTGTTT	2280
CCTGCCCCAG AAGCCGGGGT TTACTTCTCT CTGGGAGATC AGAGGCTTCA TCCTAATGTG	2340
ACCCTCGACG GGGAGAGCCT TGTGGCCACT GCCACAGCTA CAGCAAGTGA AGAACAGGAA	2400
GGCACCAAAC AGCTGATGTG CATCGTGACC CTCGGGGGCG AAAGCAGGGA GACCCAGGAA	2460
AACCTGACTG TCTACAGTAA GGGGAATCCA ACAAGACCTT CAATAGCTCA GACTGGGGCT	2520
GGGGCTGGGT CTGGGTCTGG GGCCAGAGTC TCACAAAGGC GGAGCCTATA AAGTGGGCGG	2580
GACCTCCACA CCAGAACAAG CCGGGCGGGA GAGTTCAGG GCAGGAGCAG ATAGAAGTTG	2640
GAAATTAATA GATTGGGTTG AGTTCCTGA GTGGGGAGTG AACCCACCC AATTCTCTGT	2700
CCCCAGGCTT CCCGGCTCCT CTTCTGACTT TAAGTGAGCC AGAAGCCCC GAGGGAAAGA	2760
TGGTGACCGT AAGCTGCTGG GCAGGGGCCC GAGCCCTTGT CACCTTGGAG GGAATTCCAA	2820
GGACCCTCTT ACCGGCCCCA TCTTTAACCT TATCGTATCC CCTCTGCCTC ATGCCCCGAG	2880
ACGCACCTCG GCTGGATGAC TTGGACTGTC CCAGGAGCTG GACGTGGCCA GAGGGTCCAG	2940
AGCAGACCCT CCACTGCGAG GCCCGTGGA ACCCTGAGCC CTCCGTGCAC TGTGCAAGGC	3000

CTGACGGTGG GGCGGTGCTA GCGCTGGGCC TGTTGGGTCC AGTGACCCGT GCCCTCGCGG 3060
GCACTTACCG ATGTACAGCA ATCAATGGGC AAGGCCAGGC GGTCAAGGAT GTGACCCTGA 3120
CTGTGGAATG TGAGTAGGGG GAGGTGGGCA TGCTTATCCC TTTAAGGTCA CGGAGTGTAC 3180
TGGGAGACTG GCTATACGGA AAGGAAAGAA GCCTAGGTTC AGCAGGGATT GGGAAAACAC 3240
TGAAGGAAAG TGGTGTGGTG TTTACAAACT TAACGGTGGT AACTGGGCAC GGTCTGGCAA 3300
AAACAGACAG CCAAGAGAGT GTGCCTGGGA AGCTGCAATG GGGGCTTTGT GGAATTGGT 3360
CAACAGCACC CTGAGATCTC AGGAAAGGGG CCTGAAGTTA TCTCCAGAAC CCATGTGAAG 3420
GCAGGAAGAG AGAACGCCCA CCTTTTCCTG CTCCCCCACA CCCCCCACA CATATCACAC 3480
GGAGTATATA AATAAATAAA ATGGCTCCTG CCGGAGGGAG TGAGAAGCTG TCTCCTGCAG 3540
GCTCAGAGCA GTGGTAGTGC ATGCCTTTAA TCCAGCACT CGGTAGGCAA AGGCAGGCAG 3600
ATCTCTGTGA ATGTGGGGCC AGCCTGGTCT GTACAGAGAA ATCCTGTCTC AAAACAAACC 3660
AGCAAAGAAA CAAAACCAAA ATCAATTCCA GATGCCCCAG CGCTGGACAG TGTAGGCTGC 3720
CCANGACGTA TTACTIONCT GGAGGGGACA GAGGCATCGC TTAGCTGTGT GGCACACGGG 3780
GTCCCACCAC CTAGCGTGAG CTGTGTGCGC TCTGGAAAGG AGGAAGTCAT GGAAGGGCCC 3840
CTGCGTGTGG CCCGGGAGCA CGCTGGCACT TACCGATGCG AAGCCATCAA CGCCAGGGGA 3900
TCAGCGGNCA AAAATGTGGC TGTCACGGTG GAATGTGAGT AGGGGTGGCT ACGGAAATGT 3960
CCACACCTGC GTCCTCTGTC CTCAGTGTGA ACTCCTATTT CCCTGCTTCC TAGATGGTCC 4020
CAGTTNTGAG GAGTTGGGCT GCCCCAGCAA CTGGACTTGG GTAGAAGGAT CTGGAAAAC 4080
GTTTTCTGTG GAAGTTGATG GGAAGCCGGA ACCACGCGTG GAGTGCCTGG GCTCGGAGGG 4140
TGCAAGCGAA GGGGTAGTGT TGCCCCCTGGT GTCCTCGAAC TCTGGTTCCA GAAACTCTAT 4200
GACTCCTGGT AACCTGTCAC CGGGTATTTA CCTCTGCAAC GCCACCAACC GGCATGGCTC 4260
CACAGTCAAA ACAGTCGTCG TGAGCGCGGA ATGTGAGCAG GGGCCCAGGT GGGCGGAGAG 4320
TACCGGGTGT CCCAGGATCT TTTCTTTCCC TGATGCCCCCT CTTATGGTG GCTGATCTGC 4380
AGCACCGCCA CAGATGGATG AATCCAGTTG CCCGAGTCAC CAGACATGGC TGAAGGAGC 4440
CGAGGCTACT GCGCTGGCCT GCAGTGACAG GGGNCGCCCC TCTCCACGCG TCGCTGTTC 4500
CAGGGAAGGT GCAGCCAGGC TGGAGAGGCT ACAGGTGTCC CGAGAGGATG CGGGGACCTA 4560
CCTGTGTGTG GCTACCAACG CGCATGGCAC GGATTCACGG ACCGTCAC 4620
ATGTGAGTGA GGACAGCGCT GAATGAAGAC GACTCAGACC GCCAGAAAAG TGCCTTGAGG 4680
CCTGGGATGT ATGATCCAGT GGGTAGAGTG CTCAATTAGC ACTCACTAAA ATGTATATTC 4740
TATTCCTAAT ACTCTTTAAT TTTANCCTTT GGGAGGCAGA GACAGGCAGA TCTCTGTTCC 4800
GGGATAACCT GCTCTCTGTC TAGGACAGCT TGGTCTACAG AGGGGNTACA GGCCCCCCT 4860
CCCAAGATTG NATAGCAACC CTCTGGCTCC CTGTCTCTCT 4900

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

NGAATTCCGG CGGATCGGGT AGAGCTAGTG CCTCTGCCTC CTTGGCAGCC TGTAGGTGAG	60
AACCTTCACCT TGAGCTGCAG GGTCCCAGGG GCAGGACCCC GAGCGAGCCT CACATTGACC	120
TTGCTGCGAG GCGGCCAGGA GCTGATTGCG CGAAGTTTCG TAGGCGAGCC ACCCCGAGCT	180
CGGGGTGCGA TGCTCACCGC CACGGTCTCTG GCGCGCAGAG AGGATCACAG GGCCAAATTC	240
TCATGCCTCG CGGAGCTTGA CCTGCGGCCA CACGGCTTGG GACTGTTTGC AAACAGCTCA	300
GCCCCAGAC AGCTCCGCAC GTTTGCCATG CCTCCACTTT CCCCAGCCT TATTGCCCCA	360
CGATTCTTAG AAGTGGGCTC AGAAAGGCCG GTGACTTGCA CTTTGGATGG ACTGTTTCCT	420
GCCCCAGAAG CCGGGGTTTA CCTCTCTCTG GGAGATCAGA GGCTTCATCC TAATGTGACC	480
CTCGACGGGG AGAGCCTTGT GGCCACTGCC ACAGCTACAG CAAGTGAAGA ACAGGAAGGC	540
ACCAAACAGC TGATGTGCAT CGTGACCCTC GGGGGCGAAA GCAGGGAGAC CCAGGAAAAC	600
CTGACTGTCT ACAGCTTCCC GGCTCCTCTT CTGACTTTAA GTGAGCCAGA AGCCCCGAG	660
GGAAAGATGG TGACCGTAAG CTGCTGGGCA GGGGCCCGAG CCCTTGTCAC CTTGGAGGGA	720
ATTCCAAGGA CCCTCTTACC GGCCCCATCT TTAACCTTAT CGTATCCCCT CTGCCTCATG	780
CCCGCAGACG CACCTCGGCT GGATGACTTG GACTGTCCCA GGAGCTGGAC GTGGCCAGAG	840
GGTCCAGAGC AGACCCTCCA CTGCGAGGCC CGTGGAACCC CTGAGCCCTC CGTGCACTGT	900
GCAAGGCCTG ACGGTGGGGC GGTGCTAGCG CTGGGCCTGT TGGGTCCAGT GACCCGTGCC	960
CTCGCGGGCA CTTACCGATG TACAGCAATC AATGGGCAAG GCCAGGCGGT CAAGGATGTG	1020
ACCCTGACTG TGGAATATGC CCCAGCGCTG GACAGTGTAG GCTGCCCAGA ACGTATTACT	1080
TGGCTGGAGG GGACAGAGGC ATCGCTTAGC TGTGTGGCAC ACGGGGTCCC ACCACCTAGC	1140
GTGAGCTGTG TGCGCTCTGG AAAGGAGGAA GTCATGGAAG GGCCCTGCG TTTTGGCCGG	1200
GAGCACGCTG GCACTTACCG ATGCGAAGCC ATCAACGCCA GGGGATCAGC GGCCAAAAAT	1260
GTGGCTGTCA CGGTGGAATA TGGTCCCCGG AATTC	1295

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGAATCTTGA GTGGGATGCG GGACTCCCGT GCTATTTCTT GGCGGAGGTC TTTCCTGGTC	60
CTTATGGACA CCCCTGGTTT GGGATATGGG GGCCGCTAAG ATTTTCAGAGA TGGGGTCCCT	120
AGGCTGAGCC CGCGTTTTTC CGGGCAGCGG TCGCGCTAGA ACCTTTCTGG GCGGACCTTC	180
AGCCCCGCGT GGCGCTCGTG GAGCGCGGGG GCTCGCTGTG GCTCAACTGC AGCACTAACT	240
GTCCGAGGCC GGAGCGCGGT GGYCTGGAGA CCTCGCTACG CCGAAACGGG ACCCAGAGGG	300
GTCTGCGCTG GCTGGCTCGA CAGMTGGTGG ACATCCGAGA GCCTGAAACC CAGTCGGTCT	360
GCTTCTTCCG CTGGGCGCGC CGCACACTCC AAGNGAGTGG GCTCATCCGA ACTTTCCAGC	420
GACCGGATCG GGTAGAGCTA GTGCCTCTGN CTCCTTGGA GCCTGTAGGT GAGAACTTCA	480
CCTTGAGCTG CAGGGTCCCG GGGGCAGGAC CCCGAGCGAG CCTCACATTG ACCTTGCTGC	540
GAGGCGGCCA GGAGCTGATT CGCCGAAGTT TCGTAGGCGA GCCACCCCGA GCTCGGGGTG	600
CGATGCTCAC CGCCACGGTC CTGGCGCGCA GAGAGGATCA CAGGGCCAAT TTCTCATGCC	660
TCGCGGAGCT TGACCTGCGG ACACACGGCT TGGGACTGTT TGCAAACAGC TCAGCCCCCA	720
GACAGCTCCG CACGTTTGGC ATGCCTCCAC TTTCCCCGAG CCTTATTGNC CCACGATTCT	780
TAGAAGTGGG CTCAGAAAGG CCGGTGACTT GCACTTTGGA TGGACTGTTT CTGCCCCAG	840
AAGCCGGGGT TTACCTCTCT CTGGGAGATC AGAGGCTTCA TCCTAATGTG ACCCTCGACG	900
GGGAGAGCCT TGTGGCCACT GNCACAGMTA CAGCAAGTGA AGAACAGGAA GGCACCAAAC	960
AGCTGATGTG CATCGTGACC CTCGGGGGCG AAAGCAGGGA GACCCAGGAA AACCTGACTG	1020
TCTACAGCTT CCCGGCTCCT CTTCTGACTT TAAGTGAGCC AGAAGCCCCC GAGGGAAAGA	1080
TGGTGACCGT AAGCTGCTGG GCAGGGGCCC GAGCCCTTGT CACCTTGAG GGAATTCCAG	1140
CTGCGGTCCC TGGGCAGCCC GCTGAGCTCC AGTTAAATGT CACAAAGAAT GACGACAAGC	1200
GGGGCTTCTT CTGCGACGCT GCCCTCGATG TGGACGGGGA AACTCTGAGA AAGAACCAGA	1260
GCTCTGAGCT TCGTGTTCTG TACGCACCTC GGCTGGATGA CTTGGACTGT CCCAGGAGCT	1320
GGACGTGGCC AGAGGGTCCA GAGCAGACCC TCCACTGCGA GGCCCGTGGA AACCTGAGC	1380
CCTCCGTGCA CTGTGCAAGG CCTGACGGTG GGGCGGTGCT AGCGCTGGGC CTGTTGGGTC	1440
CAGTGACCCG TGCCCTCGCG GGAACCTACC GATGTACAGC AATCAATGGG CAAGGCCAGG	1500
CGGTCAAGGA TGTGACCCTG ACTGTGGAAT ATGCCCCAGC GCTGGACAGT GTAGGCTGCC	1560
CAGAACGTAT TACTTGGCTG GAGGGGACAG AGGCATCGCT TAGCTGTGTG GCACACGGGG	1620
TCCCACCACC TAGCGTGAGC TGTGTGCGCT CTGGAAAGGA GGAAGTCATG GAAGGGCCCC	1680
TGCGTGTTGC CCGGGAGCAC GCTGGCACTT ACCGATGCGA AGCCATCAAC GNCAGGGGAT	1740
CAGCGGWCAA AAATGTGGCT GTCACGGTGG AATATGGTCC CAGTTTGGAG GAGTTGGGCT	1800

GCCCCAGYAA	CTGGACTTGG	GTAGAAGGAT	CTGGAAAAC	GTTTTCTGT	GAAGTTGATG	1860
GGAAGCCGGA	ACCACGCGTG	GAGTGCCTGG	GCTCGGAGGG	TGCAAGCGAA	GGGGTAGTGT	1920
TGCCCCCTGGT	GTCCTCGAAC	TCTGGTTCCA	GAAACTCTAT	GAATCCTGGT	AACCTGTCAC	1980
CGGGTATTTA	CCTCTGCAAC	GCCACCAACC	GGMATGGNTC	CACAGTCAAA	ACAGTCGTCG	2040
TGAGCGCGGA	ATCACCGCCA	CAGATGGATG	AATCCAGTTG	CCCAGTCAC	CAGACATGGN	2100
TGGAAGGAGC	CGAGGNTACT	GCGCTGGCCT	GCACTGCCAG	AGGNCGCCCC	TCTCCACGCG	2160
TGCGCTGTTC	CAGGGAAGGT	GCAGMCAGGC	TGGAGAGGNT	ACAGGTGTCC	CGAG	2214

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAACGCTC	CTCGGCCTCT	GGTCTNCTCT	GGNCCTGGGG	ATCCTAGGCA	TCTCAGGTAA	60
GAAGAGCCCG	CCCGTGGAGC	NAGGTGGATA	AGGCGGGGGC	GGAATTGAAG	GACCAGAGAG	120
GGCGGCCCGG	GTGTCCCCCT	CCAGGCTCCG	CCCTCTTCTA	GCTTCCCACG	CTTCTGTCAC	180
CACCTGGAGN	TCGGGGCTTC	TCCCCGTCCT	TCCTCCACCC	CAACACACCT	CAATCTTTCA	240
GANCTGAACC	CAGCACCTTT	TCTGGANTNG	GGGNNTTGCA	CCTAACCTGT	CTCAGGAGAN	300
ACTGTGGCTC	TCCTGTCCTC	TCCTGCTCTG	TNATGCCCTA	TGGTTCACAG	ACTGGCATCA	360
TCCCTATTCA	TGATCCTCAA	AGACNCCATC	TCCTCAACTG	TCATAACTCA	GAGCTCTATT	420
CCCCCTCCAC	CTGGAGCCCT	GGAACCCGGC	TTTCTAGGGC	TTTTCTCCGC	GGTTCCTTCC	480
CGGAGTTCAG	CGTTGTGGCT	TTTGTCCAA	GTTACTCAAG	TTTGGGGACA	ATCTCCTTTA	540
AGCCTTTGAC	TCAGTCTCAT	TTCCACTTTG	CTTTTGCCCC	AAGCCTCTGT	GTCTCTCCCC	600
CATTTCTTGA	CGATCTGTCA	GAGTCTTAAG	AGTGATTTGG	TTCCCCATCC	CCCCTCCAAC	660
TGGAGTCTCC	TCCTCACTAT	TGATGTGTGC	ATCTGAGACC	CCCATCCCCG	CACCGAGTTT	720
CCCCATCTCT	GTCAGTAAAG	AGCAAGGCTT	CCAGAGACAA	CCCTCTAATA	GCGCGTCAGT	780
CCCGAATCTT	GAGTGGGATG	CGGGACTCCC	GTGCTATTTT	TTGGCGGAGG	TCTTTCCTGG	840
TCCTTATGGA	CACCCCTGGT	TTGGGATATG	GGGGCCGCTA	AGATTTTCTA	GATGGGGTCC	900
CTAGGCTGAG	NCCGCGTTTT	CCCGGGCAGC	GGTCGCGCTA	GAACCTTTCT	GGGCGGACCT	960
TCAGCCCCGC	GTGGCGCTCG	TGGAGCGCGG	GGGCTCGCTG	TGGCTCAACT	GCAGCACTAA	1020
CTGTCCGAGG	CCGGAGCGCG	GTGGCCTGGA	GACCTCGCTA	CGCCGAAACG	GGACCCAGAG	1080
GGGTCTGNAC	TGNTGGCTC	GACAGCTGGT	GGACATCCGA	GANCTGAAA	CCCAGCCGGT	1140

CTGCTTCTTC CNCTGCGCGC GCCGCACACT CCAAGCGCGT GGGCTCATCC GAACTTTCCG 1200
TGAGTTCAGG GTGGGCACNC CCCTTGGGTC TCTGGACCTC CCCCTCAAGC TCCTCCCACC 1260
CGCCCTCTGA TCCTCCTGCT TGTTCGAAA GTACTACAGC TGGCTAGAGC GGAGTTTTTG 1320
GTCCCTTGCA GAGCGACCGG ATCGGGTAGA GCTAGTGCCT CTGCCTCCTT GGCAGCCTGT 1380
AGGTGAGAAC TTCACCTTGA GCTGCAGGGT CCCGGGGGCA GGACCCCGAG CGAGCCTCAC 1440
ATTGACCTTG CTGCGAGGCG GCCAGGAGCT GATTCGCCGA AGTTTCGTAG GCGAGCCACC 1500
CCGAGCTCGG GGTGCGATGC TCACCGCCAC GGTCTTGGCG CGCAGAGAGG ATCACAGGGC 1560
CAATTTCTCA TGCCTCGCGG AGCTTGACCT GCGNCCACAC GGCTTGGGAC TGTTTGCANA 1620
CAGCTCAGCC CCCAGACAGC TCCGCACGTT TGGTGAGTGT GGACCCTAAC TGACAGATTT 1680
TAAGAAGTTT AGGGCAGCCA GCGTGGTGG CATGGTGTCG TAGGCCCTAA GTCCCAGCCC 1740
AAGCAGANCT AAGNCGGATC TCTTGTGAAT TAAAAGTCTA GCTCGTCTAC ATAACGAGGN 1800
CTGCATAGTT AAATCCCCCA AAAGTCTAAG CAGCTAGCCC TTACTTCCAA CACAAGTACT 1860
AGCTTAAGTA CTTTCTCCTG TGAGCTTTTT CCTTTATGTA TTTACTCGTT GAGAGAAAAA 1920
GAGAGTGTGT GTACGTGCCT TTATGCACAT GCCGCAGTGC TTGTATGGAA GTTAAAGAAT 1980
AAGGAGGCGT TCTGCCCTTC CATCCTGTGG GTCCTAGGGG TGGTATTAGC TCCTCAGGCT 2040
TTGTTAGTNA CAAGCGCCTA GGCTTGGGGA GCCATCTCGC CCGCTCCTCT GTATCTTTAG 2100
GGTGAAACCA GACAATGCAT GCAAATTGGT TGATCAACAC TGAATGTTTA GTTCGTAAAT 2160
TCAAGCTCTG TTCTTTGTCT TCCTCAGCCA TGCCTCCACT TTCCCCCGAG CCTTATTGCC 2220
CCACGATTCT TAGAAGTGGG CTCAGAAAGG CCGGTGACKT GCACTTTGGA TGGACTGTTT 2280
CCTGCCCCAG AAGCCGGGGT TTACTTCTCT CTGGGAGATC AGAGGCTTCA TCCTAATGTG 2340
ACCCTCGACG GGGAGAGCCT TGTGGCCACT GCCACAGCTA CAGCAAGTGA AGAACAGGAA 2400
GGCACCAAAC AGCTGATGTG CATCGTGACC CTCGGGGGCG AAAGCAGGGA GACCCAGGAA 2460
AACCTGACTG TCTACAGTAA GGGGAATCCA ACAAGACCTT CAATAGCTCA GACTGGGGCT 2520
GGGGCTGGGT CTGGGTCTGG GGCCAGAGTC TCACAAAGGC GGAGCCTATA AAGTGGGCGG 2580
GACCTCCACA CCAGAACAAG CCGGGCGGGA GAGTTCCAGG GCAGGAGCAG ATAGAAGTTG 2640
GAAATTAATA GATTGGGTTG AGTTCCCTGA GTGGGGAGTG AACCCACCC AATTCTCTGT 2700
CCCCAGGCTT CCCGGCTCCT CTTCTGACTT TAAGTGAGCC AGAAGCCCC GAGGGAAAGA 2760
TGGTGACCGT AAGCTGCTGG GCAGGGGCC GAGCCCTTGT CACCTTGGAG GGAATTCCAG 2820
CTGCGGTCCC TGGGCAGCCC GCTGAGCTCC AGTTAAATGT CACAAAGAAT GACGACAAGC 2880
GGGGCTTCTT CTGCGACGCT GCCCTCGATG TGGACGGGA AACTCTGAGA AAGAACCAGA 2940
GCTCTGAGCT TCGTGTTCTG TGTGAGTGGA TGTTCACTTT ATCTCTGTGA ATTCCAAGGA 3000
CCCTCTTACC GGCCCCATCT TTAACCTTAT CGTATCCCCT CTGCCTCATG CCCGCAGACG 3060

CACCTCGGCT GGATGACTTG GACTGTCCCA GGAGCTGGAC GTGGCCAGAG GGTCCAGAGC 3120
AGACCCTCCA CTGCGAGGCC CGTGGAAACC CTGAGCCCTC CGTGCACTGT GCAAGGCCTG 3180
ACGGTGGGGC GGTGCTAGCG CTGGGCCTGT TGGGTCCAGT GACCCGTGCC CTCGCGGGCA 3240
CTTACCGATG TACAGCAATC AATGGGCAAG GCCAGGCGGT CAAGGATGTG ACCCTGACTG 3300
TGGAATGTGA GTAGGGGGAG GTGGGCATGC TTATCCCTTT AAGGTCACGG AGTGTACTGG 3360
GAGACTGGCT ATACGGAAAG GAAAGAAGCC TAGGTTACAG AGGGATTGGG AAAACACTGA 3420
AGGAAAGTGG TGTGGTGTTC ACAAACCTTA CGGTGGTAAC TGGGCACGGT CTGGCAAAAA 3480
CAGACAGCCA AGAGAGTGTG CCTGGGAAGC TGCAATGGGG GCTTTGTGGG AATTGGTCAA 3540
CAGCACCTG AGATCTCAGG AAAGGGGCCT GAAGTTATCT CCAGAACCCA TGTGAAGGCA 3600
GGAAGAGAGA ACGCCACCT TTTCTGCTC CCCCCAACCC CCCCCACAT ATCACACGGA 3660
GTATATAAAT AAATAAAATG GCTCCTGCCG GAGGGAGTGA GAAGCTGTCT CCTGCAGGCT 3720
CAGAGCAGTG GTAGTGCATG CCTTTAATCC CAGCACTCGG TAGGCAAAGG CAGGCAGATC 3780
TCTGTGAATG TGGGGCCAGC CTGGTCTGTA CAGAGAAATC CTGTCTCAA ACAAACCAGC 3840
AAAGAAACAA AACCAAAATC AATTCCAGAT GCCCCAGCGC TGGACAGTGT AGGCTGCCCA 3900
NGACGTATTA CTTGNCTGGA GGGGACAGAG GCATCGCTTA GCTGTGTGGC ACACGGGGTC 3960
CCACCACCTA GCGTGAGCTG TGTGCGCTCT GGAAAGGAGG AAGTCATGGA AGGGCCCCTG 4020
CGTGTGGCCC GGGAGCACGC TGGCACTTAC CGATGCGAAG CCATCAACGC CAGGGGATCA 4080
GCGGNCAAAA ATGTGGCTGT CACGGTGGAA TGTGAGTAGG GGTGGCTACG GAAATGTCCA 4140
CACCTGCGTC CTCTGTCCTC AGTGTGAACT CCTATTTCCC TGCTTCCTAG ATGGTCCCAG 4200
TTNTGAGGAG TTGGGCTGCC CCAGCAACTG GACTTGGGTA GAAGGATCTG GAAAACGTGT 4260
TTCCTGTGAA GTTGATGGGA AGCCGGAACC ACGCGTGGAG TCGTGGGCT CGGAGGGTGC 4320
AAGCGAAGGG GTAGTGTGTC CCCTGGTGTC CTCGAACTCT GGTTCAGAA ACTCTATGAC 4380
TCCTGGTAAC CTGTCACCGG GTATTTACCT CTGCAACGCC ACCAACCGGC ATGGCTCCAC 4440
AGTCAAAACA GTCGTCGTGA GCGCGGAATG TGAGCAGGGG CCCAGGTGGG CGGAGAGTAC 4500
CGGGTGTCCC AGGATCTTTT CTTTCCCTGA TGCCCCCTCT TATGGTGGCT GATCTGCAGC 4560
ACCGCCACAG ATGGATGAAT CCAGTTGCCC GAGTCACCAG ACATGGCTGG AAGGAGCCGA 4620
GGCTACTGCG CTGGCCTGCA GTGACAGGGG NCGCCCCCTCT CCACGCGTGC GCTGTTCCAG 4680
GGAAGGTGCA GCCAGGCTGG AGAGGCTACA GGTGTCCCGA GAGGATGCGG GGACCTACCT 4740
GTGTGTGGCT ACCAACGCGC ATGGCACGGA TTCACGGACC GTCAGTGTGG GTGTGGAATG 4800
TGAGTGAGGA CAGCGCTGAA TGAAGACGAC TCAGACCGCC AGAAAAGTGC CTTGAGGCCT 4860
GGGATGTATG ATCCAGTGGG TAGAGTGCTC AATTAGCACT CACTAAAATG TATATTCTAT 4920
TCCTAATACT CTTTAATTTT ANCCTTTGGG AGGCAGAGAC AGGCAGATCT CTGTTCCGGG 4980

ATAACCTGCT CTCTGTCTAG GACAGCTTGG TCTACAGAGG GGNTACAGGC CCCCCCTCCC 5040
AAGATTGNAT AGCAACCCTC TGGCTCCCTG TCTCTCT 5077

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

NGAATTCCGG CGGATCGGGT AGAGCTAGTG CCTCTGCCTC CTTGGCAGCC TGTAGGTGAG 60
AACTTCACCT TGAGCTGCAG GGTCCCGGGG GCAGGACCCC GAGCGAGCCT CACATTGACC 120
TTGCTGCGAG GCGGCCAGGA GCTGATTTCG CGAAGTTTCG TAGGCGAGCC ACCCCGAGCT 180
CGGGGTGCGA TGCTCACCGC CACGGTCCTG GCGCGCAGAG AGGATCACAG GGCCAATTTTC 240
TCATGCCTCG CGGAGCTTGA CCTGCGGCCA CACGGCTTGG GACTGTTTGC AAACAGCTCA 300
GCCCCAGAC AGCTCCGCAC GTTTGCCATG CCTCCACTTT CCCCAGCCT TATTGCCCCA 360
CGATTCTTAG AAGTGGGCTC AGAAAGGCCG GTGACTTGCA CTTTGATGG ACTGTTTCCT 420
GCCCCAGAAG CCGGGGTTTA CCTCTCTCTG GGAGATCAGA GGCTTCATCC TAATGTGACC 480
CTCGACGGGG AGAGCCTTGT GGCCACTGCC ACAGCTACAG CAAGTGAAGA ACAGGAAGGC 540
ACCAAACAGC TGATGTGCAT CGTGACCCTC GGGGGCGAAA GCAGGGAGAC CCAGGAAAAC 600
CTGACTGTCT ACAGCTTCCC GGCTCCTCTT CTGACTTTAA GTGAGCCAGA AGCCCCCGAG 660
GGAAAGATGG TGACCGTAAG CTGCTGGGCA GGGGCCCGAG CCCTTGTCAC CTTGGAGGGA 720
ATTCCAGCTG CGGTCCCTGG GCAGCCCGCT GAGCTCCAGT TAAATGTCAC AAAGAATGAC 780
GACAAGCGGG GCTTCTTCTG CGACGCTGCC CTCGATGTGG ACGGGGAAAC TCTGAGAAAG 840
AACCAGAGCT CTGAGCTTCG TGTTCTGTGT GAGTGGATGT TCACTTTATC TCTGTGAATT 900
CCAAGGACCC TCTTACCGGC CCCATCTTTA ACCTTATCGT ATCCCCCTG CCTCATGCCC 960
GCAGACGCAC CTCGGCTGGA TGAATTGGAC TGTCCCAGGA GCTGGACGTG GCCAGAGGGT 1020
CCAGAGCAGA CCCTCCACTG CGAGGCCCGT GGAAACCCTG AGCCCTCCGT GCACTGTGCA 1080
AGGCCTGACG GTGGGGCGGT GCTAGCGCTG GGCCTGTTGG GTCCAGTGAC CCGTGCCCTC 1140
GCGGGCACTT ACCGATGTAC AGCAATCAAT GGGCAAGGCC AGGCGGTCAA GGATGTGACC 1200
CTGACTGTGG AATATGCCCC AGCGCTGGAC AGTGTAGGCT GCCCAGAACG TATTACTTGG 1260
CTGGAGGGGA CAGAGGCATC GCTTAGCTGT GTGGCACACG GGGTCCCACC ACCTAGCGTG 1320
AGCTGTGTGC GCTCTGGAAG GGAGGAAGTC ATGGAAGGGC CCCTGCGTTT TGGCCGGGAG 1380
CACGCTGGCA CTTACCGATG CGAAGCCATC AACGCCAGGG GATCAGCGGC CAAAAATGTG 1440

GCTGTACGCG TGGAATATGG TCCCCGGAAT TC

1472

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCTCTGCCTC	CTTGGCAGCC	TGTAGGTGAG	AACTTCACCT	TGAGCTGCAG	GGTCCCGGGG	60
GCAGGACCCC	GAGCGAGCCT	CACATTGACC	TTGCTGCGAG	GCGGCCAGGA	GCTGATTCGC	120
CGAAGTTTCG	TAGGCGAGCC	ACCCCGAGCT	CGGGGTGCGA	TGCTCACCGC	CACGGTCCTG	180
GCGCGCAGAG	AGGATCACAG	GGCCAATTTT	TCATGCCTCG	CGGAGCTTGA	CCTGCGGCCA	240
CACGGCTTGG	GACTGTTTGC	AAACAGCTCA	GCCCCAGAC	AGCTCCGCAC	GTTTGCCATG	300
CCTCCACTTT	CCCCGAGCCT	TATTGCCCCA	CGATTCTTAG	AAGTGGGCTC	AGAAAGGCCG	360
GTGACTTGCA	CTTTGGATGG	ACTGTTTCCT	GCCCCAGAAG	CCGGGGTTTA	CCTCTCTCTG	420
GGAGATCAGA	GGCTTCATCC	TAATGTGACC	CTCGACGGGG	AGAGCCTTGT	GGCCACTGCC	480
ACAGCTACAG	CAAGTGAAGA	ACAGGAAGGC	ACCAAACAGC	TGATGTGCAT	CGTGACCCTC	540
GGGGGCGAAA	GCAGGGAGAC	CCAGGAAAAC	CTGACTGTCT	ACAGCTTCCC	GGCTCCTCTT	600
CTGACTTTAA	GTGAGCCAGA	AGCCCCCGAG	GGAAAGATGG	TGACCGTAAG	CTGCTGGGCA	660
GGGGCCCGAG	CCCTTGTCAC	CTTGGAGGGA	ATTCCAGCTG	CGGTCCCTGG	GCAGCCCGCT	720
GAGCTCCAGT	TAAATGTCAC	AAAGAATGAC	GACAAGCGGG	GCTTCTTCTG	CGACGCTGCC	780
CTCGATGTGG	ACGGGGAAAC	TCTGAGAAAG	AACCAGAGCT	CTGAGCTTCG	TGTTCTGTAC	840
GCACCTCGGC	TGGATGACTT	GGACTGTCCC	AGGAGCTGGA	CGTGGCCAGA	GGGTCCAGAG	900
CAGACCTCC	ACTGCGAGGC	CCGTGGAAAC	CCTGAGCCCT	CCGTGCACTG	TGCAAGGCCT	960
GACGGTGGGG	CGGTGCTAGC	GCTGGGCCTG	TTGGGTCCAG	TGACCCGTGC	CCTCGCGGGC	1020
ACTTACCGAT	GTACAGCAAT	CAATGGGCAA	GGCCAGGCGG	TCAAGGATGT	GACCCTGACT	1080
GTGGAATATG	CCCCAGCGCT	GGACAGTGTA	GGCTGCCCAG	AACGTATTAC	TTGGCTGGAG	1140
GGGACAGAGG	CATCGCTTAG	CTGTGTGGCA	CACGGGGTCC	CACCACCTAG	CGTGAGCTGT	1200
GTGCGCTCTG	GAAAGGAGGA	AGTCATGGAA	GGGCCCCCTG	GTGTGGCCCG	GGAGCACGCT	1260
GGCACTTACC	GATGCGAAGC	CATCAACGCC	AGGGGATCAG	CGGCCAAAAA	TGTGGCTGTC	1320
ACGGTGGAAT	ATGGTCCCAG	TTTTGAGGAG	TTGGGCTGCC	CCAGCAACTG	GACTTGGGTA	1380
GAAGGATCTG	GAAAACTGTT	TTCCTGTGAA	GTTGATGGGA	AGCCGGAACC	ACGCGTGGAG	1440
TGCGTGGGCT	CGGAGGGTGC	AAGCGAAGGG	GTAGTGTTGC	CCCTGGTGTC	CTCGAACTCT	1500

GGTTCAGAA ACTCTATGAC TCCTGGTAAC CTGTCACCGG GTATTTACCT CTGCAACGCC	1560
ACCAACCGGC ATGGCTCCAC AGTCAAAACA GTCGTCGTGA GCGCGGAATC ACCGCCACAG	1620
ATGGATGAAT CCAGTTGCCC GAGTCACCAG ACATGGCTGG AAGGAGCCGA GGCTACTGCG	1680
CTGGCCTGCA GTGCCAGAGG CCGCCCCCTCT CCACGCGTGC GCTGTTCCAG GGAAGGTGCA	1740
GCCAGGCTGG AGAGGCTACA GGTGTCCCGA GAGGATGCGG GGACCTACCT GTGTGTGGCT	1800
ACCAACGCGC ATGGCACGGA TTCACGGACC GTCACGTGGT GTGTGGAATA CCGGCCTGTG	1860
GTGGCTGAGC TGGCAGCCTC GCCCCAAGC GTGCGGCCTG GCGGAACTT CACTCTGACC	1920
TGCCGTGCAG AGGCCTGGCC TCCAGCCCAG ATCAGCTGGC GCGCGCCCCC GGGAGCTCTC	1980
AACCTCGGTC TCTCCAGCAA CAACAGCACG CTGAGCGTGG CGGGTGCCAT GGGCAGCCAT	2040
GGTGGCGAGT ATGAGTGCGC AGCCACCAAT GCGCATGGGC GCCACGCACG GCGCATCACG	2100
GTGCGCGTGG CCGGTCCATG GCTGTGGGTC GCTGTGGGCG GTGCGGCAGG GGGCGCGGCG	2160
CTGCTGGCCG CAGGGGCCGG CCTGGCCTTC TACGTGCAGT CCACCGCTTG CAAGAAGGGA	2220
GAGTACAACG TCCAGGAGGC TGAGAGCTCA GCGGAGGCGG TGTGTCTCAA TGGCGCGGGC	2280
GGGACACCGG GTGCAGAAGG CGGAGCAGAG ACCCCCGGCA CTGCCGAGTC ACCTGCAGAT	2340
GGCGAGGTTT TCGCCATCCA GCTGACATCT TCCTGAGCCT GTATCCAGCT CCCCCAGGGG	2400
CCTCGAAAGC ACAGGGGTGG ACGTATGTAT TGTTCACTCT CTATTTATTC AACTCCAGGG	2460
GCGTCGTCCC CGTTTTCTAC CCATTCCCTT AATAAAGTTT TTATAGGAGA AAAAAAAAAA	2520
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2550

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTCGATCA CTCGCGCTCC CCTCGCCTTC TGCGCTCTCC CCTCCCTGGC AGCGGCGGCA	60
ATGCCGGGGC CTTACCAGG GCTGCGCCGA ACGCTCCTCG GCCTCTGGGC TGCCCTGGGC	120
CTGGGGATCC TAGGCATCTC AGCGGTCGCG CTAGAACCTT TCTGGGCGGA CCTTCAGCCC	180
CGCGTGGCGC TCGTGGAGCG CGGGGGCTCG CTGTGGCTCA AC	222

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTGGAGCTG GCACCCCTGC CTCCTTGGCA GCCGGTGGGC CAGAACTTCA CCCTGCGCTG	60
CCAAGTGGAG GGTGGGTCGC CCCGGACCAG CCTCACGGTG GTGCTGCTTC GCTGGGAGGA	120
GGAGCTGAGC CGGCAGCCCG CAGTGGAGGA GCCAGCGGAG GTCAGTCCCA CTGTGCTGGC	180
CAGCAGAGAC GACCACGGAG CCCCTTTCTC ATGCCGCACA GAACTGGACA TGCAGCCCCA	240
GGGGCTGGGA CTGTTTCGTGA ACACCTCAGC CCCCCGCCAG CTCCGAACCT TT	292

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Asp Arg Val Glu Leu Val Pro Leu Pro Pro Trp Gln Pro Val Gly	1	5	10	15
Glu Asn Phe Thr Leu Ser Cys Arg Val Pro Gly Ala Gly Pro Arg Ala	20	25	30	
Ser Leu Thr Leu Thr Leu Leu Arg Gly Gly Gln Glu Leu Ile Arg Arg	35	40	45	
Ser Phe Val Gly Glu Pro Pro Arg Ala Arg Cys Ala Met Leu Thr Ala	50	55	60	
Thr Val Leu Ala Arg Arg Glu Asp His Arg Asp Asn Phe Ser Cys Leu	65	70	75	80
Ala Glu Leu Asp Leu Arg Thr His Gly Leu Gly Leu Phe Ala Asn Ser	85	90	95	
Ser Ala Pro Arg Gln Leu Arg Thr Phe	100	105		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACTCGAGG CCATGCCTCC ACTTTCC

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCATAAGCTT TATTCCACCG TGACAGCCAC

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACGTGCGGA GCTGTCTG

18

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGGAATTCG AAGCCATCAA CGCCAGG

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CATGAATTCC GAATCTTGAG TGGGATG

27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
ATAGAATTCC TCGGGACACC TG TAGCC 27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
CARGGTGACA AGGGCTCG 18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
TATGAATTCA GTTGAGCCAC AGCGAGC 27

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
CCGGGTCCTA GAGGTGGACA CGCA 24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
TGCAGTGTCT CCTGGCTCTG GTTC 24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGAAAACCG GGAGACCCGG GAGAACGTGA CCATCTACAG CTTCCCGGCA CCACTCCTGA 60
CCCTGAGCGA ACCCAGCGTC TCCGAGGGGC AGATGGTGAC AGTAACCTGC GCAGCTGGGG 120
CCCAAGCTCT GGTCACTG GAGGGAGTTC CAGCCGCGGT CCCGGGGCAG CCCGCCCAGC 180
TTCAGCTAAA TGCCACCGAG AACGACGACA GACGCAGCTT CTTCTGCGAC GCCACCCTCG 240
ATGTGGACGG GGAGACCCTG ATCAAGAACA GGAGCGCAGA GCTTCGTGTC CTATACGCTC 300
CCCGGCTAGA CGATTCTGGAC TGCCCCAGGA GTTGGACGTG GCCCCAGGGC CCAGAGCAGA 360
CGCTGCGCTG CGAGGCCCCG GGAACCCAG AACCTCAGT GCACTGTGCG CGCTCCGACG 420
GCGGGGCCGT GCTGGCTCTG GGCCTGCTGG GTCCAGTCAC TCGGGCGCTC TCAGGCACTT 480
ACCGCTGCAA GCGGCCCAAT GATCAAGGCG AGGCGGTCAA GGACGTAACG CTAACGGTGG 540
AGTACGCACC AGCGCTGGAC AGCGTGGGCT GCCCAGAACG CATTACTTGG CTGGAGGGAA 600
CAGAAGCCTC GCTGAGCTGT GTGGCGCACG GGTACCGCC GCCTGATGTG ATCTGCGTGC 660
GCTCTGGAGA ACTCGGGGCC GTCATCGAGG GGCTGTTGCG TGTGGCCCCG GAGCATGCGG 720
GCACTTACCG CTGCGAAGCC ACCAACCCTC GGGGCTCTGC GGCCAAAAT GTGGCCGTCA 780
CGGTGGAATA TGGCCCCAGG TTTGAGGAGC CGAGCTGCCC CAGCAATTGG ACATGGGTGG 840
AAGGATCTGG GCGCCTGTTT TCCTGTGAGG TCGATGGGAA GCCACAGCCA AGCGTGAAGT 900
GCGTGGGCTC CGGGGGCACC ACTGAGGGGG TGCTGCTGCC GCTGGCACC CCAGACCCTA 960
GTCCAGAGC TCCAGAATC CCTAGAGTCC TG 992

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2775 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGCCTCGC GTGGCGTTCG TGGAGCGCGG GGGCTCGCTG TGGCTGAATT GCAGCACCAA 60
CTGCCCTCGG CCGGAGCGCG GTGGCCTGGA GACCTCGCTG CGCCGAAACG GGACCCAGAG 120
GGGTTTGCGT TGTTGGCGC GGCAGCTGGT GGACATTCGC GAGCCGGAGA CTCAGCCCGT 180
CTGCTTCTTC CGCTGCGCGC GGCGCACACT ACAGGCGCGT GGGCTCATTC GCACTTTCCA 240

GCGACCAGAT CGCGTAGAGC TGATGCCGCT GCCTCCCTGG CAGCCGGTGG GCGAGAACTT	300
CACCCTGAGC TGTAGGGTCC CCGGCGCCGG GCGCCGTGCG AGCCTCACGC TGACCCTGCT	360
GCGGGGCGCC CAGGAGCTGA TCCGCCGAG CTTCGCCGGT GAACCACCCC GAGCGCGGGG	420
CGCGGTGCTC ACAGCCACGG TACTGGCTCG GAGGGAGGAC CATGGAGCCA ATTTCTCGTG	480
TCGCGCCGAG CTGGACCTGC GGCCGCACGG ACTGGGACTG TTTGAAAACA GCTCGGCCCC	540
CAGAGAGCTC CGAACCTTCT CCCTGTCTCC GGATGCCCCG CGCCTCGCTG CTCCCCGGCT	600
CTTGGAAGTT GGCTCGGAAA GGCCCGTGAG CTGCACTCTG GACGGACTGT TTCCAGCCTC	660
AGAGGCCAGG GTCTACCTCG CACTGGGGGA CCAGAATCTG AGTCCTGATG TCACCCTCGA	720
AGGGGACGCA TTCGTGGCCA CTGCCACAGC CACAGCTAGC GCAGAGCAGG AGGGTGCCAG	780
GCAGCTGGTC TGCAACGTCA CCCTGGGGGG CGAAAACCGG GAGACCCGGG AGAACGTGAC	840
CATCTACAGC TTCCCGGCAC CACTCCTGAC CCTGAGCGAA CCCAGCGTCT CCGAGGGGCA	900
GATGGTGACA GTAACCTGCG CAGCTGGGGC CCAAGCTCTG GTCACACTGG AGGGAGTTCC	960
AGCCGCGGTC CCGGGGCAGC CCGCCCAGCT TCAGCTAAAT GCCACCGAGA ACGACGACAG	1020
ACGCAGCTTC TTCTGCGACG CCACCCTCGA TGTGGACGGG GAGACCCTGA TCAAGAACAG	1080
GAGCGCAGAG CTTCGTGTCC TATACGCTCC CCGGCTAGAC GATTCCGACT GCCCCAGGAG	1140
TTGGACGTGG CCCGAGGGCC CAGAGCAGAC GCTGCGCTGC GAGGCCCCGCG GGAACCCAGA	1200
ACCCTCAGTG CACTGTGCGC GCTCCGACGG CGGGGCCGTG CTGGCTCTGG GCCTGCTGGG	1260
TCCAGTCACT CGGGCGCTCT CAGGCACCTA CCGTGCAAG GCGGCCAATG ATCAAGGCGA	1320
GGCGGTCAAG GACGTAACGC TAACGGTGGA GTACGCACCA GCGCTGGACA GCGTGGGCTG	1380
CCCAGAACGC ATTACTTGGC TGGAGGGAAC AGAAGCCTCG CTGAGCTGTG TGGCGCACGG	1440
GGTACCGCCG CCTGATGTGA TCTGCGTGCG CTCTGGAGAA CTCGGGGCCG TCATCGAGGG	1500
GCTGTTGCGT GTGGCCCCGG AGCATGCGGG CACTTACCGC TGCGAAGCCA CCAACCCTCG	1560
GGGCTCTGCG GCCAAAAATG TGGCCGTCAC GGTGGAATAT GGCCCCAGGT TTGAGGAGCC	1620
GAGCTGCCCC AGCAATTGGA CATGGGTGGA AGGATCTGGG CGCCTGTTTT CCTGTGAGGT	1680
CGATGGGAAG CCACAGCCAA GCGTGAAGTG CGTGGGCTCC GGGGGCACCA CTGAGGGGGT	1740
GCTGCTGCCG CTGGCACCCC CAGACCCTAG TCCCAGAGCT CCCAGAATCC CTAGAGTCCT	1800
GGCACCCGGT ATCTACGTCT GCAACGCCAC CAACCGCCAC GGCTCCGTGG CCAAAACAGT	1860
CGTCGTGAGC GCGGAGTCGC CACCGGAGAT GGATGAATCT ACCTGCCCAA GTCACCAGAC	1920
GTGGCTGGAA GGGGCTGAGG CTTCCGCGCT GGCCTGCGCC GCGGGGGTGC GCCCTTCCCC	1980
AGGAGTGCGC TGCTCTCGGG AAGGCATCCC ATGGCCTGAG CAGCAGCGCG TGTCCCGAGA	2040
GGACGCGGGC ACTTACCACT GTGTGGCCAC CAATGCGCAT GGCACGGACT CCCGGACCGT	2100
CACTGTGGGC GTGGAATACC GGCCAGTGGT GGCCGAACCT GCTGCCTCGC CCCCTGGAGG	2160

CGTGCGCCCA GGAGGAAACT TCACGTTGAC CTGCCGCGCG GAGGCCTGGC CTCCAGCCCA	2220
GATCAGCTGG CGCGCGCCCC CGAGGGCCCT CAACATCGGC CTGTCGAGCA ACAACAGCAC	2280
ACTGAGCGTG GCAGGCGCCA TGGGAAGCCA CGGCGGCGAG TACGAGTGCG CACGCACCAA	2340
CGCGCACGGG CGCCACGCGC GGCGCATCAC GGTGCGCGTG GCCGGTCCGT GGCTATGGGT	2400
CGCCGTGGGC GGCGCGGCGG GGGGCGCGGC GCTGCTGGCC GCGGGGGCCG GCCTGGCCTT	2460
CTACGTGCAG TCCACCGCCT GCAAGAAGGG CGAGTACAAC GTGCAGGAGG CCGAGAGCTC	2520
AGGCGAGGCC GTGTGTCTGA ACGGAGCGGG CGGCGGCGCT GCGGGGGCGG CAGGCGCGGA	2580
GGGCGGACCC GAGGCGGCGG GGGGCGCGGC CGAGTCGCCG GCGGAGGGCG AGGTCTTCGC	2640
CATACAGCTG ACATCGGCGT GAGCCCCTC CCCTCTCCGC GGGCCGGGAC GGGGGGAGG	2700
CTCACACGGG GGCTTATTTA TTGCTTTATT TATTTACTTA TTCATTTATT TATGTATTCA	2760
ACTCCAAGGG AATTC	2775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGCGCTCTCC TCGCCTCCTG TGCTTTCCCC GCGCGGCGGA TGCCAGGGCC TTCGCCAGGG	60
CTGCGCCGGG CGCTACTCGG CCTCTGGGCT GCTCTGGGCC TGGGGCTCTT CGGCCTCTCA	120
GCGGTCTCGC AGGAGCCCTT CTGGGCGGAC CTGCAGCCTC GCGTGGCGTT CGTGGAGCGC	180
GGGGGCTCGC TGTGGCTGAA TTGCAGCACC AACTGCCCTC GGCCGGAGCG CGGTGGCCTG	240
GAGACCTCGC TGCGCCGAAA CGGGACCCAG AGGGGTTTGC GTTGGTTGGC GCGGCAGCTG	300
GTGGACATTC GCGAGCCGGA GACTCAGCCC GTCTGCTTCT TCCGCTGCGC GCGGCGCACA	360
CTACAGGCGC GTGGGCTCAT TCGCACTTTC CAGCGACCAG ATCGCGTAGA GCTGATGCCG	420
CTGCCTCCCT GGCAGCCGCT GGGCGAGAAC TTCACCTGA GCTGTAGGGT CCCCAGCGCC	480
GGGCCCCGTG CGAGCCTCAC GCTGACCCTG CTGCGGGGCG CCCAGGAGCT GATCCGCCGC	540
AGCTTCGCCG GTGAACCACC CCGAGCGCGG GGCGCGGTGC TCACAGCCAC GGTACTGGCT	600
CGGAGGGAGG ACCATGGAGC CAATTTCTCG TGTCGCGCCG AGCTGGACCT GCGGCCGCAC	660
GGACTGGGAC TGTTTGAAAA CAGCTCGGCC CCCAGAGAGC TCCGAACCTT CTCCCTGTCT	720
CCGGATGCCC CGCGCCTCGC TGCTCCCCGG CTCTTGGAAG TTGGCTCGGA AAGGCCCGTG	780
AGCTGCACTC TGGACGGA CTGTTCCAGCC TCAGAGGCCA GGGTCTACCT CGCACTGGGG	840
GACCAGAATC TGAGTCCTGA TGTCACCCTC GAAGGGGACG CATTTCGTGGC CACTGCCACA	900

GCCACAGCTA GCGCAGAGCA GGAGGGTGCC AGGCAGCTGG TCTGCAACGT CACCCTGGGG	960
GGCGAAAACC GGGAGACCCG GGAGAACGTG ACCATCTACA GCTTCCCGGC ACCACTCCTG	1020
ACCCTGAGCG AACCCAGCGT CTCCGAGGGG CAGATGGTGA CAGTAACCTG CGCAGCTGGG	1080
GCCCAAGCTC TGGTCACACT GGAGGGAGTT CCAGCCGCGG TCCCAGGGCA GCCCGCCAG	1140
CTTCAGCTAA ATGCCACCGA GAACGACGAC AGACGCAGCT TCTTCTGCGA CGCCACCCTC	1200
GATGTGGACG GGGAGACCCT GATCAAGAAC AGGAGCGCAG AGCTTCGTGT CCTATACGCT	1260
CCCCGGCTAG ACGATTCTGA CTGCCCCAGG AGTTGGACGT GGCCCGAGGG CCCAGAGCAG	1320
ACGCTGCGCT GCGAGGCCCC CGGGAACCCA GAACCCTCAG TGCACTGTGC GCGCTCCGAC	1380
GGCGGGGCGG TGCTGGCTCT GGGCCTGTG GGTCCAGTCA CTCGGGCGCT CTCAGGCACT	1440
TACCGCTGCA AGGCGGCCAA TGATCAAGGC GAGGCGGTCA AGGACGTAAC GCTAACGGTG	1500
GAGTACGCAC CAGCGCTGGA CAGCGTGGGC TGCCCAGAAC GCATTACTTG GCTGGAG	1557

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 40..2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGCGCTCTCC TCGCCTCCTG TGCTTTCCCC GCCGCGGCG ATG CCA GGG CCT TCG	54
Met Pro Gly Pro Ser	
1 5	
CCA GGG CTG CGC CGG GCG CTA CTC GGC CTC TGG GCT GCT CTG GGC CTG	102
Pro Gly Leu Arg Arg Ala Leu Leu Gly Leu Trp Ala Ala Leu Gly Leu	
10 15 20	
GGG CTC TTC GGC CTC TCA GCG GTC TCG CAG GAG CCC TTC TGG GCG GAC	150
Gly Leu Phe Gly Leu Ser Ala Val Ser Gln Glu Pro Phe Trp Ala Asp	
25 30 35	
CTG CAG CCT CGC GTG GCG TTC GTG GAG CGC GGG GGC TCG CTG TGG CTG	198
Leu Gln Pro Arg Val Ala Phe Val Glu Arg Gly Gly Ser Leu Trp Leu	
40 45 50	
AAT TGC AGC ACC AAC TGC CCT CGG CCG GAG CGC GGT GGC CTG GAG ACC	246
Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg Gly Gly Leu Glu Thr	
55 60 65	
TCG CTG CGC CGA AAC GGG ACC CAG AGG GGT TTG CGT TGG TTG GCG CGG	294
Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu Arg Trp Leu Ala Arg	
70 75 80 85	

CAG	CTG	GTG	GAC	ATT	CGC	GAG	CCG	GAG	ACT	CAG	CCC	GTC	TGC	TTC	TTC	342
Gln	Leu	Val	Asp	Ile	Arg	Glu	Pro	Glu	Thr	Gln	Pro	Val	Cys	Phe	Phe	
				90					95					100		
CGC	TGC	GCG	CGG	CGC	ACA	CTA	CAG	GCG	CGT	GGG	CTC	ATT	CGC	ACT	TTC	390
Arg	Cys	Ala	Arg	Arg	Thr	Leu	Gln	Ala	Arg	Gly	Leu	Ile	Arg	Thr	Phe	
			105					110					115			
CAG	CGA	CCA	GAT	CGC	GTA	GAG	CTG	ATG	CCG	CTG	CCT	CCC	TGG	CAG	CCG	438
Gln	Arg	Pro	Asp	Arg	Val	Glu	Leu	Met	Pro	Leu	Pro	Trp	Gln	Pro		
		120					125					130				
GTG	GGC	GAG	AAC	TTC	ACC	CTG	AGC	TGT	AGG	GTC	CCC	GGC	GCC	GGG	CCC	486
Val	Gly	Glu	Asn	Phe	Thr	Leu	Ser	Cys	Arg	Val	Pro	Gly	Ala	Gly	Pro	
	135					140					145					
CGT	GCG	AGC	CTC	ACG	CTG	ACC	CTG	CTG	CGG	GGC	GCC	CAG	GAG	CTG	ATC	534
Arg	Ala	Ser	Leu	Thr	Leu	Thr	Leu	Leu	Arg	Gly	Ala	Gln	Glu	Leu	Ile	
150					155					160					165	
CGC	CGC	AGC	TTC	GCC	GGT	GAA	CCA	CCC	CGA	GCG	CGG	GGC	GCG	GTG	CTC	582
Arg	Arg	Ser	Phe	Ala	Gly	Glu	Pro	Pro	Arg	Ala	Arg	Gly	Ala	Val	Leu	
				170					175					180		
ACA	GCC	ACG	GTA	CTG	GCT	CGG	AGG	GAG	GAC	CAT	GGA	GCC	AAT	TTC	TCG	630
Thr	Ala	Thr	Val	Leu	Ala	Arg	Arg	Glu	Asp	His	Gly	Ala	Asn	Phe	Ser	
			185					190					195			
TGT	CGC	GCC	GAG	CTG	GAC	CTG	CGG	CCG	CAC	GGA	CTG	GGA	CTG	TTT	GAA	678
Cys	Arg	Ala	Glu	Leu	Asp	Leu	Arg	Pro	His	Gly	Leu	Gly	Leu	Phe	Glu	
		200					205					210				
AAC	AGC	TCG	GCC	CCC	AGA	GAG	CTC	CGA	ACC	TTC	TCC	CTG	TCT	CCG	GAT	726
Asn	Ser	Ser	Ala	Pro	Arg	Glu	Leu	Arg	Thr	Phe	Ser	Leu	Ser	Pro	Asp	
	215					220					225					
GCC	CCG	CGC	CTC	GCT	GCT	CCC	CGG	CTC	TTG	GAA	GTT	GGC	TCG	GAA	AGG	774
Ala	Pro	Arg	Leu	Ala	Ala	Pro	Arg	Leu	Leu	Glu	Val	Gly	Ser	Glu	Arg	
230				235						240					245	
CCC	GTG	AGC	TGC	ACT	CTG	GAC	GGA	CTG	TTT	CCA	GCC	TCA	GAG	GCC	AGG	822
Pro	Val	Ser	Cys	Thr	Leu	Asp	Gly	Leu	Phe	Pro	Ala	Ser	Glu	Ala	Arg	
				250					255					260		
GTC	TAC	CTC	GCA	CTG	GGG	GAC	CAG	AAT	CTG	AGT	CCT	GAT	GTC	ACC	CTC	870
Val	Tyr	Leu	Ala	Leu	Gly	Asp	Gln	Asn	Leu	Ser	Pro	Asp	Val	Thr	Leu	
			265					270					275			
GAA	GGG	GAC	GCA	TTC	GTG	GCC	ACT	GCC	ACA	GCC	ACA	GCT	AGC	GCA	GAG	918
Glu	Gly	Asp	Ala	Phe	Val	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Ser	Ala	Glu	
		280					285					290				
CAG	GAG	GGT	GCC	AGG	CAG	CTG	GTC	TGC	AAC	GTC	ACC	CTG	GGG	GGC	GAA	966
Gln	Glu	Gly	Ala	Arg	Gln	Leu	Val	Cys	Asn	Val	Thr	Leu	Gly	Gly	Glu	
	295				300					305						
AAC	CGG	GAG	ACC	CGG	GAG	AAC	GTG	ACC	ATC	TAC	AGC	TTC	CCG	GCA	CCA	1014
Asn	Arg	Glu	Thr	Arg	Glu	Asn	Val	Thr	Ile	Tyr	Ser	Phe	Pro	Ala	Pro	
310					315				320					325		
CTC	CTG	ACC	CTG	AGC	GAA	CCC	AGC	GTC	TCC	GAG	GGG	CAG	ATG	GTG	ACA	1062
Leu	Leu	Thr	Leu	Ser	Glu	Pro	Ser	Val	Ser	Glu	Gly	Gln	Met	Val	Thr	
				330					335					340		

GTA Val	ACC Thr	TGC Cys	GCA Ala 345	GCT Ala	GGG Gly	GCC Ala	CAA Gln	GCT Ala 350	CTG Leu	GTC Val	ACA Thr	CTG Leu	GAG Glu 355	GGA Gly	GTT Val	1110
CCA Pro	GCC Ala 360	GCG Ala	GTC Val	CCG Pro	GGG Gly	CAG Gln	CCC Pro 365	GCC Ala	CAG Gln	CTT Leu	CAG Gln	CTA Leu 370	AAT Asn	GCC Ala	ACC Thr	1158
GAG Glu	AAC Asn 375	GAC Asp	GAC Asp	AGA Arg	CGC Arg	AGC Ser 380	TTC Phe	TTC Phe	TGC Cys	GAC Asp	GCC Ala 385	ACC Thr	CTC Leu	GAT Asp	GTG Val	1206
GAC Asp 390	GGG Gly	GAG Glu	ACC Thr	CTG Leu	ATC Ile 395	AAG Lys	AAC Asn	AGG Arg	AGC Ser	GCA Ala 400	GAG Glu	CTT Leu	CGT Arg	GTC Val	CTA Leu 405	1254
TAC Tyr	GCT Ala	CCC Pro	CGG Arg 410	CTA Leu	GAC Asp	GAT Asp	TCG Ser	GAC Asp	TGC Cys 415	CCC Pro	AGG Arg	AGT Ser	TGG Trp	ACG Thr 420	TGG Trp	1302
CCC Pro	GAG Glu	GGC Gly	CCA Pro 425	GAG Glu	CAG Gln	ACG Thr	CTG Leu	CGC Arg 430	TGC Cys	GAG Glu	GCC Ala	CGC Arg	GGG Gly 435	AAC Asn	CCA Pro	1350
GAA Glu	CCC Pro 440	TCA Ser	GTG Val	CAC His	TGT Cys	GCG Ala	CGC Arg 445	TCC Ser	GAC Asp	GGC Gly	GGG Gly	GCC Ala 450	GTG Val	CTG Leu	GCT Ala	1398
CTG Leu	GGC Gly 455	CTG Leu	CTG Leu	GGT Gly	CCA Pro	GTC Val 460	ACT Thr	CGG Arg	GCG Ala	CTC Leu	TCA Ser 465	GGC Gly	ACT Thr	TAC Tyr	CGC Arg	1446
TGC Cys 470	AAG Lys	GCG Ala	GCC Ala	AAT Asn	GAT Asp 475	CAA Gln	GGC Gly	GAG Glu	GCG Ala	GTC Val 480	AAG Lys	GAC Asp	GTA Val	ACG Thr	CTA Leu 485	1494
ACG Thr	GTG Val	GAG Glu	TAC Tyr 490	GCA Ala	CCA Pro	GCG Ala	CTG Leu	GAC Asp	AGC Ser 495	GTG Val	GGC Gly	TGC Cys	CCA Pro	GAA Glu 500	CGC Arg	1542
ATT Ile	ACT Thr	TGG Trp	CTG Leu 505	GAG Glu	GGA Gly	ACA Thr	GAA Glu	GCC Ala 510	TCG Ser	CTG Leu	AGC Ser	TGT Cys	GTG Val 515	GCG Ala	CAC His	1590
GGG Gly	GTA Val	CCG Pro 520	CCG Pro	CCT Pro	GAT Asp	GTG Val	ATC Ile 525	TGC Cys	GTG Val	CGC Arg	TCT Ser	GGA Gly 530	GAA Glu	CTC Leu	GGG Gly	1638
GCC Ala	GTC Val 535	ATC Ile	GAG Glu	GGG Gly	CTG Leu	TTG Leu 540	CGT Arg	GTG Val	GCC Ala	CGG Arg	GAG Glu 545	CAT His	GCG Ala	GGC Gly	ACT Thr	1686
TAC Tyr 550	CGC Arg	TGC Cys	GAA Glu	GCC Ala	ACC Thr 555	AAC Asn	CCT Pro	CGG Arg	GGC Gly	TCT Ser 560	GCG Ala	GCC Ala	AAA Lys	AAT Asn	GTG Val 565	1734
GCC Ala	GTC Val	ACG Thr	GTG Val	GAA Glu 570	TAT Tyr	GGC Gly	CCC Pro	AGG Arg	TTT Phe 575	GAG Glu	GAG Glu	CCG Pro	AGC Ser	TGC Cys 580	CCC Pro	1782
AGC Ser	AAT Asn	TGG Trp	ACA Thr 585	TGG Trp	GTG Val	GAA Glu	GGA Gly	TCT Ser 590	GGG Gly	CGC Arg	CTG Leu	TTT Phe 595	TCC Ser	TGT Cys	GAG Glu	1830

GTC Val	GAT Asp	GGG Gly 600	AAG Lys	CCA Pro	CAG Gln	CCA Pro	AGC Ser 605	GTG Val	AAG Lys	TGC Cys	GTG Val	GGC Gly 610	TCC Ser	GGG Gly	GGC Gly	1878
ACC Thr	ACT Thr 615	GAG Glu	GGG Gly	GTG Val	CTG Leu 620	CTG Leu	CCG Pro	CTG Leu	GCA Ala	CCC Pro	CCA Pro 625	GAC Asp	CCT Pro	AGT Ser	CCC Pro	1926
AGA Arg 630	GCT Ala	CCC Pro	AGA Arg	ATC Ile	CCT Pro 635	AGA Arg	GTC Val	CTG Leu	GCA Ala	CCC Pro 640	GGT Gly	ATC Ile	TAC Tyr	GTC Val	TGC Cys 645	1974
AAC Asn	GCC Ala	ACC Thr	AAC Asn 650	CGC Arg	CAC His	GGC Gly	TCC Ser	GTG Val	GCC Ala 655	AAA Lys	ACA Thr	GTC Val	GTC Val	GTG Val 660	AGC Ser	2022
GCG Ala	GAG Glu	TCG Ser 665	CCA Pro	CCG Pro	GAG Glu	ATG Met	GAT Asp	GAA Glu 670	TCT Ser	ACC Thr	TGC Cys	CCA Pro	AGT Ser 675	CAC His	CAG Gln	2070
ACG Thr	TGG Trp 680	CTG Leu	GAA Glu	GGG Gly	GCT Ala	GAG Glu	GCT Ala 685	TCC Ser	GCG Ala	CTG Leu	GCC Ala	TGC Cys 690	GCC Ala	GCC Ala	CGG Arg	2118
GGT Gly 695	CGC Arg	CCT Pro	TCC Ser	CCA Pro	GGA Gly 700	GTG Val	CGC Arg	TGC Cys	TCT Ser	CGG Arg	GAA Glu 705	GGC Gly	ATC Ile	CCA Pro	TGG Trp	2166
CCT Pro 710	GAG Glu	CAG Gln	CAG Gln	CGC Arg	GTG Val 715	TCC Ser	CGA Arg	GAG Glu	GAC Asp 720	GCG Ala	GGC Gly	ACT Thr	TAC Tyr	CAC His	TGT Cys 725	2214
GTG Val	GCC Ala	ACC Thr	AAT Asn 730	GCG Ala	CAT His	GGC Gly	ACG Thr	GAC Asp 735	TCC Ser	CGG Arg	ACC Thr	GTC Val	ACT Thr	GTG Val 740	GGC Gly	2262
GTG Val	GAA Glu	TAC Tyr 745	CGG Arg	CCA Pro	GTG Val	GTG Val	GCC Ala 750	GAA Glu 750	CTT Leu	GCT Ala	GCC Ala	TCG Ser	CCC Pro 755	CCT Pro	GGA Gly	2310
GGC Gly 760	GTG Val	CGC Arg	CCA Pro	GGA Gly	GGA Gly	AAC Asn	TTC Phe 765	ACG Thr	TTG Leu	ACC Thr	TGC Cys	CGC Arg 770	GCG Ala	GAG Glu	GCC Ala	2358
TGG Trp 775	CCT Pro	CCA Pro	GCC Ala	CAG Gln	ATC Ile	AGC Ser 780	TGG Trp	CGC Arg	GCG Ala	CCC Pro	CCG Pro 785	AGG Arg	GCC Ala	CTC Leu	AAC Asn	2406
ATC Ile 790	GGC Gly	CTG Leu	TCG Ser	AGC Ser	AAC Asn 795	AAC Asn	AGC Ser	ACA Thr	CTG Leu	AGC Ser 800	GTG Val	GCA Ala	GGC Gly	GCC Ala	ATG Met 805	2454
GGA Gly	AGC Ser	CAC His	GGC Gly 810	GGC Gly	GAG Glu	TAC Tyr	GAG Glu	TGC Cys	GCA Ala 815	CGC Arg	ACC Thr	AAC Asn	GCG Ala	CAC His 820	GGG Gly	2502
CGC Arg	CAC His	GCG Ala	CGG Arg 825	CGC Arg	ATC Ile	ACG Thr	GTG Val	CGC Arg 830	GTG Val	GCC Ala	GGT Gly	CCG Pro	TGG Trp 835	CTA Leu	TGG Trp	2550
GTC Val	GCC Ala	GTG Val 840	GGC Gly	GGC Gly	GCG Ala	GCG Ala	GGG Gly 845	GGC Gly	GCG Ala	GCG Ala	CTG Leu	CTG Leu 850	GCC Ala	GCG Ala	GGG Gly	2598

100355413991

GCC GGC CTG GCC TTC TAC GTG CAG TCC ACC GCC TGC AAG AAG GGC GAG	2646
Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys Lys Gly Glu	
855 860 865	
TAC AAC GTG CAG GAG GCC GAG AGC TCA GGC GAG GCC GTG TGT CTG AAC	2694
Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val Cys Leu Asn	
870 875 880 885	
GGA GCG GGC GGC GGC GCT GGC GGG GCG GCA GGC GCG GAG GGC GGA CCC	2742
Gly Ala Gly Gly Gly Ala Gly Gly Ala Ala Gly Ala Glu Gly Gly Pro	
890 895 900	
GAG GCG GCG GGG GGC GCG GCC GAG TCG CCG GCG GAG GGC GAG GTC TTC	2790
Glu Ala Ala Gly Gly Ala Ala Glu Ser Pro Ala Glu Gly Glu Val Phe	
905 910 915	
GCC ATA CAG CTG ACA TCG GCG TGAGCCCGCT CCCCTCTCCG CGGGCCGGGA	2841
Ala Ile Gln Leu Thr Ser Ala	
920 925	
CGCCCCCAG ACTCACACGG GGGCTTATTT ATTGCTTTAT TTATTTACTT ATTCATTTAT	2901
TTATGTATTC AACTCCAAGG GAATTC	2927

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Pro	Gly	Pro	Ser	Pro	Gly	Leu	Arg	Arg	Ala	Leu	Leu	Gly	Leu	Trp
1				5					10					15	
Ala	Ala	Leu	Gly	Leu	Gly	Leu	Phe	Gly	Leu	Ser	Ala	Val	Ser	Gln	Glu
		20						25					30		
Pro	Phe	Trp	Ala	Asp	Leu	Gln	Pro	Arg	Val	Ala	Phe	Val	Glu	Arg	Gly
		35					40					45			
Gly	Ser	Leu	Trp	Leu	Asn	Cys	Ser	Thr	Asn	Cys	Pro	Arg	Pro	Glu	Arg
	50					55					60				
Gly	Gly	Leu	Glu	Thr	Ser	Leu	Arg	Arg	Asn	Gly	Thr	Gln	Arg	Gly	Leu
65					70					75					80
Arg	Trp	Leu	Ala	Arg	Gln	Leu	Val	Asp	Ile	Arg	Glu	Pro	Glu	Thr	Gln
				85					90					95	
Pro	Val	Cys	Phe	Phe	Arg	Cys	Ala	Arg	Arg	Thr	Leu	Gln	Ala	Arg	Gly
			100					105					110		
Leu	Ile	Arg	Thr	Phe	Gln	Arg	Pro	Asp	Arg	Val	Glu	Leu	Met	Pro	Leu
		115					120					125			
Pro	Pro	Trp	Gln	Pro	Val	Gly	Glu	Asn	Phe	Thr	Leu	Ser	Cys	Arg	Val
		130				135					140				

Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly
145 150 155 160

Ala Gln Glu Leu Ile Arg Arg Ser Phe Ala Gly Glu Pro Pro Arg Ala
165 170 175

Arg Gly Ala Val Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His
180 185 190

Gly Ala Asn Phe Ser Cys Arg Ala Glu Leu Asp Leu Arg Pro His Gly
195 200 205

Leu Gly Leu Phe Glu Asn Ser Ser Ala Pro Arg Glu Leu Arg Thr Phe
210 215 220

Ser Leu Ser Pro Asp Ala Pro Arg Leu Ala Ala Pro Arg Leu Leu Glu
225 230 235 240

Val Gly Ser Glu Arg Pro Val Ser Cys Thr Leu Asp Gly Leu Phe Pro
245 250 255

Ala Ser Glu Ala Arg Val Tyr Leu Ala Leu Gly Asp Gln Asn Leu Ser
260 265 270

Pro Asp Val Thr Leu Glu Gly Asp Ala Phe Val Ala Thr Ala Thr Ala
275 280 285

Thr Ala Ser Ala Glu Gln Glu Gly Ala Arg Gln Leu Val Cys Asn Val
290 295 300

Thr Leu Gly Gly Glu Asn Arg Glu Thr Arg Glu Asn Val Thr Ile Tyr
305 310 315 320

Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Ser Val Ser Glu
325 330 335

Gly Gln Met Val Thr Val Thr Cys Ala Ala Gly Ala Gln Ala Leu Val
340 345 350

Thr Leu Glu Gly Val Pro Ala Ala Val Pro Gly Gln Pro Ala Gln Leu
355 360 365

Gln Leu Asn Ala Thr Glu Asn Asp Asp Arg Arg Ser Phe Phe Cys Asp
370 375 380

Ala Thr Leu Asp Val Asp Gly Glu Thr Leu Ile Lys Asn Arg Ser Ala
385 390 395 400

Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Ser Asp Cys Pro
405 410 415

Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu Arg Cys Glu
420 425 430

Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Ser Asp Gly
435 440 445

Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu
450 455 460

Ser Gly Thr Tyr Arg Cys Lys Ala Ala Asn Asp Gln Gly Glu Ala Val
465 470 475 480

Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val
 485 490 495
 Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu
 500 505 510
 Ser Cys Val Ala His Gly Val Pro Pro Pro Asp Val Ile Cys Val Arg
 515 520 525
 Ser Gly Glu Leu Gly Ala Val Ile Glu Gly Leu Leu Arg Val Ala Arg
 530 535 540
 Glu His Ala Gly Thr Tyr Arg Cys Glu Ala Thr Asn Pro Arg Gly Ser
 545 550 555 560
 Ala Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Arg Phe Glu
 565 570 575
 Glu Pro Ser Cys Pro Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Arg
 580 585 590
 Leu Phe Ser Cys Glu Val Asp Gly Lys Pro Gln Pro Ser Val Lys Cys
 595 600 605
 Val Gly Ser Gly Gly Thr Thr Glu Gly Val Leu Leu Pro Leu Ala Pro
 610 615 620
 Pro Asp Pro Ser Pro Arg Ala Pro Arg Ile Pro Arg Val Leu Ala Pro
 625 630 635 640
 Gly Ile Tyr Val Cys Asn Ala Thr Asn Arg His Gly Ser Val Ala Lys
 645 650 655
 Thr Val Val Val Ser Ala Glu Ser Pro Pro Glu Met Asp Glu Ser Thr
 660 665 670
 Cys Pro Ser His Gln Thr Trp Leu Glu Gly Ala Glu Ala Ser Ala Leu
 675 680 685
 Ala Cys Ala Ala Arg Gly Arg Pro Ser Pro Gly Val Arg Cys Ser Arg
 690 695 700
 Glu Gly Ile Pro Trp Pro Glu Gln Gln Arg Val Ser Arg Glu Asp Ala
 705 710 715 720
 Gly Thr Tyr His Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg
 725 730 735
 Thr Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala
 740 745 750
 Ala Ser Pro Pro Gly Gly Val Arg Pro Gly Gly Asn Phe Thr Leu Thr
 755 760 765
 Cys Arg Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro
 770 775 780
 Pro Arg Ala Leu Asn Ile Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser
 785 790 795 800
 Val Ala Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Arg
 805 810 815

Thr Asn Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala
820 825 830
Gly Pro Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala
835 840 845
Leu Leu Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala
850 855 860
Cys Lys Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu
865 870 875 880
Ala Val Cys Leu Asn Gly Ala Gly Gly Gly Ala Gly Gly Ala Ala Gly
885 890 895
Ala Glu Gly Gly Pro Glu Ala Ala Gly Gly Ala Ala Glu Ser Pro Ala
900 905 910
Glu Gly Glu Val Phe Ala Ile Gln Leu Thr Ser Ala
915 920

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTACTTACAG GATCCGCGGT CTCGCAGGAG CCCTTCTGGG CGGACCTACA GCCTGCGTGG 60
CGTTC 65

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTCTCTCG AGGATGGTCA CGTTCTCCCG G 31

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATTTCTGGAT CCTACAGCTT CCCGGCACCA CTC

33

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTTCTCTCG AGTTCCACGC CCACAGTGAC GG

32

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCTTTG AGCCCTGAAA GTCGAGGTTG CAGTGAGCCT TGATCGTGCC ACTGCACTCC	60
AGCCTGGGGG ACAGAGCACG ACCCTGTCTC CAAAAATAAA ATAAAAATAA AAATAAATAT	120
TGGCGGGGGA ACCCTCTGGA ATCAATAAAG GCTTCCTTAA CCAGCCTCTG TCCTGTGACC	180
TAAGGGTCCG CATTACTGCC CTTCTTCGGA GGAAGTGGTT TGTTCCTTGT GTTGTGTTG	240
TTTTTGCGAT CACTTTCTCC AAGTTCCTTG TCTCCCTGAG GGCACCTGAG GTTTCCTCAC	300
TCAGGGCCCA CCTGGGGTCC CGAAGCCCCA GACTCTGTGT ATCCCCAGCG GGTGTCACAG	360
AAACCTCTCC TTCTGCTGGC CTTATCGAGT GGGATCAGCG CGGCCGGGGA GAGCCACGGG	420
CAGGGGCGGG GTGGGGTTCA TGGTATGGCT TTCCTGATTG GCGCCGCCGC CACCACGCGG	480
CAGCTCTGAT TGGATGTTAA GTTTCCTATC CCAGCCCCAC CTTCAGACCC TGTGCTTTCC	540
TGGAGGCCAA ACAACTGTGG AGCGAGAAGT CATCTCCAAA ATAACCTACC ACGCTGGAGT	600
GAGACCACGA ATGGTGGGGA GGGGAGGGTC CCACGGACAT ATTGAGGGAC GTGGATACGC	660
AGAAGAGGTA TCCATGTGGT GGCAGCCGGG AAGGGGTGAT CAGATGGTCC ACAGGGAATA	720
TCACAACTC GAATTCTGAC GATGTTCTGG TAGTCACCCA GCCAGATGAG CGCATGGAGT	780
TGGCGGTGGG GGGTGTCAAA GCTTGGGGCC CGGAAGCGGA GTCAAAAGCA TCACCCTCGG	840
TCCCTTGTTT TCGCGTGGAT GTCAGGGCCT CCACCCACCG AGCAGAAGGC GGAAGTCAAGG	900
GCGCTCCAGG GTGGCTCGAG CTCACACACG CTGAGTAGAC ACGTGCCCGC TGCACCCTGG	960
GTAAATACAG ACCCGGAGCC GAGCGGATTC TAATTTAGAC GCCCGCGAAC GCTGCGCGCA	1020
CGCACACGTG TCCTCGGCTC GCTGGCACTT TCGTCCCGCC CCCTCCGTCG CGTGCCGGAG	1080

CTGACCCGGA GGGGTGCTTA GAGGTATGGC TCCGCGGGGT CAAAAGGAGA AGGATCAGTG 1140
 AGAGAGGATC CCCACACCCT CCCCTAGAAC TGTCCTTTCC CCATCCAGTG CCTCCCAAAT 1200
 CTCTCTTAGT CCCCAAATGT ATCCCCGCCC TAAGGGGCGC TGGTGGGAGG AGCTAAATGT 1260
 GGGGGCGGAG CTCGGAGTCC AGCTTATTAT CATGGCATCT CAGCCAGGGC TGGGGTAGGG 1320
 GTTTGGGAAG GGCAACCCAG CATCCCCCGA TCCCAGAGTC GCGGCCGGGG ATGACGCGAG 1380
 AGAGCGTGGT CGCCCCCAGA AGGCCCTGGG CCATCATGCC GGCCTCCACG TAGACCCAG 1440
 GGGTCGCTCA CTCCTGCCAG CTCGCCTTCA CCAAGGCCAG GAGCTTAGCG CACGCTCGCC 1500
 TCCCGCCCCC CCGCCGCCTC TGCCGCCGCC CCCTCCTTGG AAACCAAGTT ACCAACGTTA 1560
 AACCAATCCC CAAGCGCAAC TCTGTCTCCC CCACACCCCA CCCGCCGCGC CGCGCGGAGC 1620
 CGTCCTCTAG CCCAGCTCCT CGGCTCGCGC TCTCTCGCC TCCTGTGCTT TCCCCGCCGC 1680
 GGCGATG 1687

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAGAACTAAG CTTACAGGAG GCGAGGAGAG CGCGAG 36

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAACAATGCT AGCCAAGCGC AACTCTGTCT C 31

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAACAATGCT AGCCTTGGA ACCAAGTTAC C 31

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAACAATGCT AGCAGGAGCT TAGCGCACGC TCG

33

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CAACAATGCT AGCCATGCCG GCCTCCACGT AG

32

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAACAATGCT AGCGTCCAGC TTATTATCAT G

31

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAACAATGCT AGCCTTAGTC CCCAAATGTA TC

32

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

33